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92044

From: Gibbs, Terra  
 Sent: Tuesday, April 22, 2003 10:53 AM  
 To: STIC-Biotech/ChemLib  
 Subject: Sequence search request...

P

Could you please do a regular search of SEQ ID NO:3 of USSN 09/918026?

Terra Gibbs #79523  
 AU 1635  
 Mailbox 11E12  
 306-3221

THANK YOU!

Point of Contact:  
 Beverly Shears  
 Technical Info. Specialist  
 M1 1E05 Tel: 308-4994

Searcher: \_\_\_\_\_  
 Phone: \_\_\_\_\_  
 Location: \_\_\_\_\_  
 Date Picked Up: \_\_\_\_\_  
 Date Completed: \_\_\_\_\_  
 Searcher Prep/Review: \_\_\_\_\_  
 Clerical: \_\_\_\_\_  
 Online time: \_\_\_\_\_

TYPE OF SEARCH:  
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 AA Sequences: \_\_\_\_\_  
 Structures: \_\_\_\_\_  
 Bibliographic: \_\_\_\_\_  
 Litigation: \_\_\_\_\_  
 Full text: \_\_\_\_\_  
 Patent Family: \_\_\_\_\_  
 Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
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 DIALOG: \_\_\_\_\_  
 Questel/Orbit: \_\_\_\_\_  
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 Other (specify): \_\_\_\_\_

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GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 03:25:07 ; Search time 2934 Seconds  
(without alignments)  
15563.157 Million cell updates/sec

Title: US-09-918-026A-3

Perfect score: 1569

Sequence: 1 atggagccggcgccggccg.....cttggtccgtgccataccatg 1569

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl :

1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_cm.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pi.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
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40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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5	1115	71.1	2170	10	BC025931 Mus muscu
6	1112.4	70.9	1607	10	AF078751 Mus muscu
7	421.4	26.9	3041	10	S81092 acyl-coenzy
8	421.4	26.9	3697	10	MUSACT
9	412.2	26.3	1750	10	D86373 Rattus norv
10	410.4	26.2	1673	9	AF053336 Chloroceb
11	407.2	26.0	4011	9	HUMACYLCOA
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16	405.6	25.9	4011	6	AR080271 Sequence
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19	404	25.7	2746	9	AK026611 Homo sapi
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30	194.6	12.4	919	4	OCU65393 Oryctolagus
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# ALIGNMENTS

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AF099031

LOCUS

DEFINITION Homo sapiens acyl Co-A: cholesterol acyltransferase-2 (ACAT2) mRNA,  
complete cds.

ACCESSION AF099031

VERSION AF099031.2 GI:4878036

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

REFERENCE

AUTHORS

1569 bp mRNA linear PRI 11-SEP-2000  
Homo sapiens acyl Co-A: cholesterol acyltransferase-2 (ACAT2) mRNA,  
complete cds.  
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Homo sapiens.  
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1 (bases 1 to 1569)  
Chang,C.C., Sakashita,N., Ornvald,K., Lee,O., Chang,E.T., Dong,R.,  
Lin,S., Lee,C.Y., Strom,S.C., Kashyap,R., Fung,J.J., Farese,R.V.

Jr., Patoiseau, J.F., Delhon, A. and Chang, T.Y.:  
Immunological quantitation and localization of ACAT-1 and ACAT-2 in  
human liver and small intestine  
J. Biol. Chem. 275 (36), 28083-28092 (2000)  
20428724  
10846185  
PUBMED  
REFERENCE  
2 (bases 1 to 1569)  
Lee, O., Farese, R.V. Jr. and Chang, T.Y.  
Human ACAT-2 nucleotide sequence  
Unpublished  
JOURNAL  
3 (bases 1 to 1569)  
Lee, O., Farese, R.V. Jr. and Chang, T.Y.  
Direct Submission  
Submitted (15-OCT-1998) Biochemistry, Dartmouth, HB 7200, Hanover,  
NH 03755, USA  
REFERENCE  
4 (bases 1 to 1569)  
Lee, O., Farese, R.V. Jr. and Chang, T.Y.  
Direct Submission  
Submitted (20-MAY-1999) Biochemistry, Dartmouth, HB 7200, Hanover,  
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REMARK  
Sequence update by submitter  
On May 20, 1999 this sequence version replaced gi:3892234.  
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## source

## gene

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REFERENCE  
AUTHORS

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JOURNAL

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LOCUS AF078751  
DEFINITION Mus musculus acyl coenzyme A:cholesterol acyltransferase-2  
ACCESSION AF078751  
VERSION AF078751.1 GI:3746693  
KEYWORDS Mus musculus  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1607)  
AUTHORS Cases, S., Novak, S., Zheng, Y. W., Myers, H. M., Lear, S. R., Sande, E., Welch, C. B., Lusis, A. J., Spencer, T. A., Krause, B. R., Erickson, S. K. and Farese, R. V. Jr.  
TITLE ACAT-2, a second mammalian acyl-CoA:cholesterol acyltransferase.  
JOURNAL Its cloning, expression, and characterization  
MEDLINE J. Biol. Chem. 273 (41), 26755-26764 (1998)  
PUBMED 98434591  
REFERENCE 2 (bases 1 to 1607)  
AUTHORS Farese, R. V. Jr.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-1998) Gladstone Institute, 2550 23rd Street, San Francisco, CA 94110, USA  
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ORIGIN

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QY 265 TCCCTGAGCAGCAGCAGGACCATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAG 324  
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## RESULT 7

S81092

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REMARK

FEATURES

Source

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CDS

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146..1768

Mus sp. peritoneal macrophages.

Mus sp.

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 3041)

Green,S., Steinberg,D. and Quehenberger,O.

Cloning and expression in Xenopus oocytes of a mouse homologue of

the human acyl-coenzyme A: cholesterol acyltransferase and its

potential role in metabolism of oxidized LDL

Biochem. Biophys. Res. Commun. 218 (3), 924-929 (1996)

96158986

8579615

GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 175976] from the original journal article.

This sequence comes from Fig. 3A.

Location/Qualifiers

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/gene="acyl-coenzyme A:cholesterol acyltransferase, ACAT"

146..1768

Mus sp. peritoneal macrophages.

Mus sp.

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 3041)

Green,S., Steinberg,D. and Quehenberger,O.

Cloning and expression in Xenopus oocytes of a mouse homologue of

the human acyl-coenzyme A: cholesterol acyltransferase and its

potential role in metabolism of oxidized LDL

Biochem. Biophys. Res. Commun. 218 (3), 924-929 (1996)

96158986

8579615

GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 175976] from the original journal article.

This sequence comes from Fig. 3A.

Location/Qualifiers

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1..3041

/gene="acyl-coenzyme A:cholesterol acyltransferase, ACAT"

146..1768



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LOCUS
DEFINITION
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mRNA, complete cds.
ACCESSION
L42293
VERSION
L42293.1 GI:1066809
KEYWORDS
acyl-coenzyme A:cholesterol acyltransferase.
SOURCE
Mus musculus cDNA to mRNA.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
1 (bases 1 to 3697)
REFERENCE
Gelmen,P.J., Oka,K., Sullivan,M., Chang,C.C., Chang,T.Y., and
Chan,L.
TITLE
Tissue-specific expression and cholesterol regulation of:
acylcoenzyme A:cholesterol acyltransferase (ACAT) in mice.
Molecular cloning of mouse ACAT cDNA, chromosomal localization, and
regulation of ACAT in vivo and in vitro
J. Biol. Chem. 270 (44), 26192-26201 (1995)
95064687
PUBMED
7592824
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477 AAGTGGACCATCAGAACAAATTTACACATGTTTCATTGGCCCTCCTCATCATCTTCATCC 536  
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407 TCAGCACCTCGCCATCGACTTCATTGATGAGCGAGGCTGCTCTGAGGTGTTTCACCTAC 466  
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RESULT 10	AF053336	1673 bp	linear	PRI 12-JUL-1999
LOCUS	AF053336	Chloroebus aethiops acyl-CoA:cholesterol acyltransferase 1 (ACAT1)		
DEFINITION		mRNA		
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ACCESSION	AF053336	1. GI:3582756		
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
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		Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;		
		Cercopithecinae; Cercopithecus.		
REFERENCE		1 (bases 1 to 1673)		
AUTHORS		Anderson,R.A., Joyce,C., Davis,M., Reagan,J.W., Clark,M.,		
		Shelness,G.S. and Rudel,L.L.		
TITLE		Identification of a form of acyl-CoA:cholesterol acyltransferase		
		specific to liver and intestine in nonhuman primates		
JOURNAL		J. Biol. Chem. 273 (41), 26747-26754 (1998)		
MEDLINE		98434590		
PUBMED		9756918		
REFERENCE		2 (bases 1 to 1673)		
AUTHORS		Anderson,R.A., Joyce,C., Davis,M., Reagan,J., Clark,M., Shelness,G.		
		and Rudel,L.L.		

TITLE Direct Submission  
JOURNAL Submitted (11-MAR-1998) Internal Medicine, Wake Forest University  
School of Medicine, Medical Center Boulevard, Winston-Salem, NC  
27157, USA

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DEFINITION complete cds.

ACCESSION L21934

VERSION L21934.2

KEYWORDS GI:4878021

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 4011)

Chang,C.C., Huh,H.Y., Cadigan,K.M. and Chang,T.Y.

Molecular cloning and functional expression of human acyl-coenzyme

A:cholesterol acyltransferase cDNA in mutant Chinese hamster ovary

cells

J. Biol. Chem. 268 (28), 20747-20755 (1993)

94012607

PUBMED 8407899  
REFERENCE 2 (bases 1 to 4011)  
AUTHORS Chang, C.C. and Chang, T.Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-NOV-1993) Biochemistry Dept., Dartmouth Medical School, Hanover, NH 03755, USA  
REFERENCE 3 (bases 1 to 4011)  
AUTHORS Chang, C.C. and Chang, T.Y.  
TITLE Direct Submission  
JOURNAL Submitted (20-MAY-1999) Biochemistry Dept., Dartmouth Medical School, Hanover, NH 03755, USA  
REMARK Sequence update by submitter  
COMMENT On May 20, 1999 this sequence version replaced gi:409203.  
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RESULT 12

CGU47320

LOCUS

DEFINITION

Cricetulus griseus acyl-coA:cholesterol acyltransferase mRNA,

complete cds.

ACCESSION

U47320

VERSION

U47320.1

KEYWORDS

GT:1408465

SOURCE

ORGANISM

Cricetulus griseus.

Cricetulus griseus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

Cricetulus.

CGU47320 3024 bp mRNA linear ROD:28-JUL-1996

Cricetulus griseus acyl-coA:cholesterol acyltransferase mRNA,

complete cds.

ACCESSION

U47320

VERSION

U47320.1

KEYWORDS

GT:1408465

SOURCE

ORGANISM

Cricetulus griseus.

Cricetulus griseus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

Cricetulus.

REFERENCE 1 (bases 1 to 3024)  
 AUTHORS Cao, G., Goldstein, J.L. and Brown, M.S.  
 TITLE Complementation of mutation in acyl-CoA:cholesterol acyltransferase (ACAT) fails to restore sterol regulation in ACAT-defective sterol-resistant hamster cells  
 J. Biol. Chem. 271 (24), 14642-14648 (1996)  
 JOURNAL 96278939  
 MEDLINE 8662991  
 PUBMED 8662991  
 REFERENCE 2 (bases 1 to 3024)  
 AUTHORS Cao, G., Brown, M.S. and Goldstein, J.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JAN-1996) Guoqing Cao, Molecular Genetics, University of Texas Southwestern, 5323 Harry Hines Blvd., Dallas, TX 75235, USA

## FEATURES

source

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## RESULT 13

AF354622

LOCUS

DEFINITION

AF354622

AF354622.1

GI:18028941

cds

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1528 bp mRNA linear PRI 17-APR-2002  
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 AF354622  
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 GI:18028941  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 1 (bases 1 to 1528)  
 Stauter, R.L., Walker, A., Ryder, O.A., Lyons-Weiler, M. and



Hedges, S.B.  
Human and ape molecular clocks and constraints on paleontological hypotheses  
J. Hered. 92 (6), 469-474 (2001)  
21945518  
MEDLINE  
11948213  
PUBMED  
REFERENCE 2 (bases 1 to 1528)  
Hedges, S.B.  
Direct Submission  
Submitted (27-FEB-2001) Department of Biology, The Pennsylvania State University, 208 Mueller Lab, University Park, PA 16802, USA  
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ORIGIN

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Best Local Similarity 59.5%; Pred. No. 5e-71;  
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DB 502 CTACATTTTCAGTTCCCTATTTCTGTTTCAACATTTGGGCGACCTGATAGCAAGATT 561  
QY 587 CGAGGCGCTGGGTGCGCTTTAGCCCGCCACGCGGTGGTCTCTGGCGCGTGGCGG 646  
DB 562 CTCATCCGCTGATCGGTCTCTCTCTCCATGCTTTCTTTTCATGATCTTCAGATTGG 621  
QY 647 TCC-----ACGTGGCGGTGGAGCATGACCTCCCGCGCGCTCCCGCT 688  
DB 622 TTCTAGGTTTTGGACCAACATATGTTGTTGGCATATACATGCCACGCTTCCCGGT 681  
QY 689 GTGTCCTGGTCTCGACAGGTTAGTTCTCTGATGAAAGCTACTCTCTCTCTGAGAGG 748  
DB 682 TCATCATATTATCGACGAGATTGGTTTGTGATGAAGGCGCCACTCATTTGTCAGAGAGA 741

QY 749 CTGTGCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGATCCAGGCCCGCCAGTTTCTCCA 808  
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QY 809 G-----CTACCTCTACTTCTCTCTGCCCAACATCATCTACAGGAGAGATTACCT 861  
DB 801 GTCAACCAAGTATTGTTACTTCTTATTTGCTCTCTACCTTATCTACCTGACAGTATCCC 860  
QY 862 AGGAGCGCTTATGTTCAGTGTGAATATGTGSCCAAGAACTTTGGCCAGGCGCTGGAGT 921  
DB 861 AGAATCCCACTGTAAGATGGGTTATGCTGATGAAGTTTGACAGGCTTTGGTTGTC 920  
QY 922 GTGCTCTATGCTGCTTCTATCTCTGGCGGCTCTGTGTTCTCTGTTTGGCAACATGAGC 981  
DB 921 TTTTCTCTATGTACTACATCTTTGAAAGGCTTTGTGCCCTTGTTCGGAATATCAAA 980  
QY 982 CGAGAGCGCTTACGACCGCTGCTGCTCTCTATCTCTGATGATGACCACTGTCGAGGC 1041  
DB 981 CAGGAGCGCTTACGCGCTGCTGCTCTGCTCTATGTTGTTAACTCTCATCTTCCAGGT 1040  
QY 1042 ATCTTCTATGCTGCTCATCTTCTTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1101  
DB 1041 GTGCTGATCT 1100  
QY 1102 GAGATGCTACGATTTGGAGACAGATGTTCTACCGGAGCTGGTGGAACTCAACGCTCTTC 1161  
DB 1101 GAGATGTTACGCTTTGCTGACAGATGTTCTATAAGGATTTGGTGGAACTCCACGCTCATAC 1160  
QY 1162 TCAACTACTACCGCATTTGGAAGCTGGTGGTCCATGCTGCTGCTGCTGCTGCTGCTGCTAT 1221  
DB 1161 TCCAATCTATTAAGAACTTGAATGTTGGTGGTCCATGCTGCTGCTGCTGCTGCTGCTAT 1220  
QY 1222 CAGATGGCTGCGGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281  
DB 1221 AAGCACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1280  
QY 1282 CTGCTCTCCGAGTGGCCCATGATATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1341  
DB 1281 GCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1340  
QY 1342 GTCATGCTGATACCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401  
DB 1341 GTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1400  
QY 1402 CGACCGCGCGGCGGAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1461  
DB 1401 CGGAAAGCGGATTTGGAATGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1460  
QY 1462 CAGTCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521  
DB 1461 TTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1520  
QY 1522 ACTTCT 1528  
DB 1521 ACATTT 1527

RESULT 14  
BC028940  
LOCUS  
DEFINITION  
Homo sapiens, sterol O-acyltransferase (acyl-Coenzyme A:  
cholesterol acyltransferase) 1, clone MGC:29940 IMAGE:4991365,  
mRNA, complete cds.  
ACCESSION  
BC028940.1 GI:20809439  
VERSION  
BC028940.1  
KEYWORDS  
MGC.  
SOURCE  
Homo sapiens.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 3407)  
AUTHORS  
Strausberg, R.  
TITLE  
Direct Submission





RESULT 15  
LOCUS AR053912 4011 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5834283.  
ACCESSION AR053912  
VERSION AR053912.1 GI:5978774  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 4011)  
AUTHORS Chang, F.-Y. and Chang, C.C.-Y.  
TITLE Acyl coenzyme A:cholesterol acyltransferase (ACAT)  
JOURNAL Patent: US 5834283-A 3 10-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..4011  
BASE COUNT 1056 a 792 c 839 g 1324 t  
ORIGIN  
Query Match 25.98; Score 405.6; DB 6; Length 4011;  
Best Local Similarity 58.98; Pred. No. 5e-71;  
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;  
Qy 287 CATCCCTGGGAAACAGAAAGTTTTTCATCCGCAAGTCCCTGCTTGATGAGCTGATGG 346  
Db 1737 CACCTCCAGAACAGGAAAGATTTTATTGCAAGCGCTCTCTCTAGATGAACCTGCTG 1796.  
Qy 347 AGGTGAGCATTTCCGACCATCTACACATGTTTCATCGCTGGGCTGTGTCTTCATCA 406  
Db 1797 AAGTGGACCATCAGAACATATACATGTTTTATTGCGCTCTCTCTCTCTTTATCC 1856  
Qy 407 TCAGACCCCTGGCATCGACTTCATGATGAGGCGAGCTCTGCTGGAGTTGACCTAC 466  
Db 1857 TCAGACACTGTAGTATACATGATGAAGGAAGCTGGTGTGATGATCGCTCC 1916  
Qy 467 TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTCTGT 526  
Db 1917 TGCTCTATGCTTTGGCAAAATTCCTACCGTGTGTTGGAACCTGGTGATCATGTCTCTGT 1976  
Qy 527 CCACCTGTTGGCGCGTACAGGCGCTTACGCTGTGGGCGAGGGGACCTGGAGCAGG 586  
Db 1977 CTACATTTTCAGTTCCCTTAATTTCTGTTTCAACATTTGGCGCACTGGCTATAGCAAGAGTT 2036  
Qy 587 CGACGGGCTCGGCTGTGCGCTTTTAGCGCCACCGCTGTGGCTGTGCTGCGCGTGGCGG 646  
Db 2037 CTCATCCGCTGATCGGTTCTCTTCCATGGCTTCTTTTCATGATCTTCAGATGGAG 2096  
Qy 647 TCC-----ACGTGGCCGTGGAGCATCAGTCCCGCGGCGCTCCCGTT 688  
Db 2097 TTCATAGGTTTGGACCAACATATGTTGTTAGCATATACACTGCCACAGCTTCCCGGT 2156  
Qy 689 GTGCTCGGCTTCGAGCAGGTTAGTTCCTGTATGAAGACTACTCTCTCTGAGAGAGG 748  
Db 2157 TCATCATATATTCGAGCAGATTCGTTTGTAAATGAAGGCCCACTCAATTTGTCAGAGAGA 2216  
Qy 749 CTGTCCTGGGATCTTCGTCGCCAGCAGGTGAGGGATCCAGGCCCCCAGTTTCTCCA 808  
Db 2217 ACGTGCCTCGGGTACTAAAT--TCAGCTAAGGAGAAATCAAGCACTGTTCCAAATACCTACA 2275  
Qy 809 G-----CTACCTCTACTTCTCTCTGCGCAACACTCATCTACAGGGAGACTTACCGT 861  
Db 2276 GTCACACAGTATTGTACTCTTATTTGCTCTCTACCTTATCTACCGTGACAGCTATCCC 2335  
Qy 862 AGGACGCCCTATGTCAGGTGGAATATGTGGCCAAAGACTTTGGCCAGGCCCTGGGATGT 921  
Db 2336 AGGAATCCCACTGTAAGATGGGTTATGTCGCTATGAAGTTTGCACAGGCTCTTTGGTTGC 2395  
Qy 922 GTGCTCTATGCGCTTCATCCTCGGGCGCTCTGTGTTCCTGTCTTTGCCAACATGAGC 981  
Db 2396 TTTTCTATGTACTACATCTTTGAAAGGCTTTGTGCCCTTGTGCGCAATATCAAA 2455

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Qy 1102 GAGATGCTACGATTTGGAGACAGGATGTTCTACCGGAGTGGTGAACCTCAACGCTCTTC 1161  
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Qy 1222 CAGATGGGCTGGGCTCTCTTGGTGGCCCGGCGGAGGTAGCCATGCTGGGTGTGTC 1281  
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Qy 1462 CAGGTCAGCCTGTACTGCGCAGGAGTGTACGACGCGGCACTGCTGCTTACCCAGGCA 1521  
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Search completed: April 28, 2003, 08:26:02  
Job time : 2971 secs

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GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 04:50:18 ; Search time 262 Seconds  
(without alignments)  
13486.204 Million cell updates/sec

Title: US-09-918-026a-3

Perfect score: 1569

Sequence: 1 atggagccagcgggccgcg.....cttgctcgtccatcacctag 1569

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1564.2	99.7	2040	21 AAA76170	Human ACAT Related
2	1425.8	90.9	1509	21 AAZ57360	Human acyl CoA:cho
3	1112.4	70.9	1607	21 AAZ57359	Mouse acyl CoA:cho
4	645	41.1	1082	19 AAV01534	Human acylcoenzyme
5	407.2	26.0	4011	15 AAQ63212	Acetyl coenzyme A:
6	404	25.7	3649	19 AAV01536	Human acylcoenzyme
7	394.6	25.1	3650	19 AAT96368	Human acyl-coenzym
8	191.8	12.2	455	19 AAV01545	Acylcoenzyme A:cho
9	172	11.0	1885	23 ABL13759	Drosophila melanog

10	172	11.0	2657	23 ABL15694	Drosophila melanog
11	172	11.0	4360	23 ABL13758	Drosophila melanog
12	134.6	8.6	996	15 AAQ63210	Acetyl coenzyme A:
13	95	6.1	983	19 AAV01539	Human acylcoenzyme
14	95	6.1	993	22 ABA06413	Human cDNA SEQ ID
15	95	6.1	1521	19 AAV01533	Human acylcoenzyme
16	95	6.1	1895	21 AAZ57360	Human acyl CoA:cho
17	95	6.1	1895	21 AAZ5383	DNA encoding a pro
18	95	6.1	1976	21 AA76169	Human ACAT Related
19	93.8	6.0	542	22 AAS27552	cDNA encoding nove
20	92.4	5.9	774	22 AAS27244	cDNA encoding nove
21	88.2	5.6	447	21 AAC28517	Human secreted pro
22	81.4	5.2	452	24 ABL1686	Human ovarian can
23	81.4	5.2	1650	21 AAZ49452	Mouse diacylglycer
24	80	5.1	1122	20 AA30335	DNA encoding a hum
25	79.8	5.1	1766	21 AA88846	Rat acyl CoA:chole
26	79.8	5.1	1766	21 AAZ45385	Acyl-CoA:cholester
27	79.8	5.1	1766	22 AAS01105	Rat sterol acyltra
28	70.2	4.5	1359	21 AA48935	Corn diacylglycer
29	69.6	4.4	978	21 AA48934	Corn diacylglycer
30	69.6	4.4	1281	21 AA48933	Corn diacylglycer
31	65	4.1	901	21 AA48936	Corn diacylglycer
32	64.8	4.1	1587	21 AA48938	Rice diacylglycer
33	60.6	3.9	5574	24 AAS63338	Chemically pretrea
34	60.4	3.8	1975	21 AA48942	Wheat diacylglycer
35	60	3.8	60	24 ABN36849	Human spliced tran
36	59	3.8	1942	21 AA48939	Soybean diacylglyc
37	55.8	3.6	4170	22 AA69416	Human immune/haema
38	55.4	3.5	519	21 AA88843	M. alpina acyl CoA
39	55.4	3.5	519	21 AAZ45380	Acyl-CoA:cholester
40	55.4	3.5	519	22 AAZ45380	Mortierella alpina
41	52.8	3.4	10732	21 AA10594	Gene encoding a su
42	50	3.2	1888	21 AA48932	Arabidopsis diacyl
43	50	3.2	1904	21 AA51482	A. thaliana diacyl
44	50	3.2	1942	21 AA88835	Arabidopsis acyl C
45	50	3.2	1942	21 AAZ45371	Acyl-CoA:cholester

ALIGNMENTS

RESULT 1

AAA76170  
ID AAA76170 standard; DNA; 2040 BP.

XX  
AC  
AAA76170;

XX  
DT 14-DEC-2000 (first entry)

XX  
DE Human ACAT Related Gene Product 2 ARGP2 coding sequence.

XX  
DE Human; ACAT Related Gene Product 2; ARGP2; enzyme;  
KW acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1; ACAT2;  
KW sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;  
KW DGAT; ss.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
CDS 52..1620  
FT FT  
FT FT  
FT FT

XX  
FT /tag= a  
FT /product= "Human ARGP2"

XX  
PN US6100077-A.

XX  
XX 08-AUG-2000.

XX  
PD Mouse acyl CoA:cho

XX  
PF Human acylcoenzyme

XX  
XX 98US-0165042.

XX  
PR 01-OCT-1998;

XX  
PR 01-OCT-1998; 98US-0165042.

XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX



KW antilipemic; hypercholesterolaemia; hypertriglyceridaemia;  
 KW hyperlipidaemia; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1509

FT FT /\*tag= a

FT FT /product= "ACAT-2"

FT FT /transl\_except= (pos:571..573,aa:Xaa)

XX /note= "Xaa is unspecified"

PN W09967368-A1.

XX XX

XX 29-DEC-1999.

XX 16-JUN-1999; 99WO-US13683.

XX 23-JUN-1998; 98US-0090354.

PR 08-JUN-1999; 99US-0328857.

XX XX

XX (REGC ) UNIV CALIFORNIA.

XX XX

PI Cases S, Farese RV, Novak S, Erickson SK;

XX WPI; 2000-106291/09.

DR P-PSDB; AAV67953.

XX XX

PT Novel polypeptide, useful to treat conditions associated with elevated

PT cholesterol ester levels e.g. hypercholesterolemia

XX XX

PS Example; Page 52; 57pp; English.

XX XX

CC The present sequence encodes the human acyl CoA:cholesterol  
 CC acyltransferase designated ACAT-2. ACAT-2 polypeptides can be  
 CC administered therapeutically, especially by expressing encoding  
 CC polynucleotides, to treat individuals in need of ACAT-2 polypeptide.  
 CC They may especially be administered to treat disease conditions  
 CC associated with elevated cholesterol ester levels e.g.  
 CC hypercholesterolaemia or hyperlipidaemia (including  
 CC hypertriglyceridaemia), since ACAT-2 catalyses the esterification of  
 CC cholesterol with fatty acyl CoA substrates. The polypeptides can also  
 CC be used to diagnose diseases related to polypeptide expression or  
 CC activity, by analysing for polypeptide presence or amount in a sample.  
 CC They are useful to screen for compounds inhibiting or activating the  
 CC polypeptide, which can be included in pharmaceutical compositions and  
 CC administered therapeutically to treat conditions associated with ACAT-2;  
 CC inhibitory agents can especially be used to inhibit ACAT-2 activity,  
 CC especially therapeutically, and especially agents which selectively  
 CC inhibit ACAT-2 and not prior art ACAT-1.

XX XX

SQ Sequence 1509 BP; 260 A; 457 C; 439 G; 351 T; 2 other;

XX XX

Query Match 90.9%; Score 1425.8; DB 21; Length 1509;

Best Local Similarity 95.8%; Pred. No. 0;

Matches 1500; Conservative 0; Mismatches 9; Indels 60; Gaps 1;

1 ATGGAGCCAGCGGGCCCTCTCGCTCAGAGGACAGAGGGCTGGGAGGGAGCGG 60

1 ATGGAGCCAGCGGGCCCTCTCGCTCAGAGGACAGAGGGCTGGGAGGGAGCGG 60

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61 GAGCGCCAAACCTCTGGAGATGGAACACATGAGAGCCACAGAGCCCGGACTTGGTACAA 120

121 TGGACCGACACATGGAGGCTGTGAAGGACAAATTCGTGGAGCAAGCGCAGGACAACTG 180

121 TGGACCGACACATGGAGGCTGTGAAGGACAAATTCGTGGAGCAAGCGCAGGACAACTG 180

181 AGGAGCTGCTGGATCGGGCCATGCGGGAGGCTATACAACTCCTACCCATCACAGACAAA 240

181 AGGAGCTGCTGGATCGGGCCATGCGGGAGGCTATACAACTCCTACCCATCACAGACAAA 240

1021 CTGCATGCCAGCTGGCCAGGCATCTTCATGCTGCTGCTCATCTCTTTGGCTTCTCCAT 1080

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961 CTGCATGCCAGCTGGCCAGGCATCTTCATGCTGCTGCTCATCTCTTTGGCTTCTCCAT 1020

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1021 TGCTGGCTCAACGCTTTGGCCAGATGCTACGATTTGGAGACAGAGTGTTCACCGGAC 1080

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1081 TGTGGAACTCAACGCTCTTCTCAACTACTACCGCATTTGGAACGTTGGTGGTCCATGAC 1140

1081 TGTGGAACTCAACGCTCTTCTCAACTACTACCGCATTTGGAACGTTGGTGGTCCATGAC 1140

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1261 GTAGCCATGCTGGGTGTCTCCGAGTGGCCCATGAGTATATCTTCTGCTTC 1320

1201 GTAGCCATGCTGGGTGTCTCCGAGTGGCCCATGAGTATATCTTCTGCTTC 1260

1201 GTAGCCATGCTGGGTGTCTCCGAGTGGCCCATGAGTATATCTTCTGCTTC 1260

1321 GTCTGGGGTCTTCTTCTATCCCGTATGCTGATATCTTCTTGTGATGGAGGAATGTG 1380

1321 GTCTGGGGTCTTCTTCTATCCCGTATGCTGATATCTTCTTGTGATGGAGGAATGTG 1380

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241 CCTCTGCCCCACCTCCCCAGGTTCTTGGAGCAGGACCCAGGAGCCATCCCTGGGGAAA 300

301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGGAGGTGCAGCATTTTC 360

301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGGAGGTGCAGCATTTTC 360

276 -----TGAGCTGATGGAGGTGCAGCATTTTC 300

361 CGCACCATCTACACATGTTTCATCGCTGGCTGTGCTCTTTCATCATCAGCACCTCGGCC 420

361 CGCACCATCTACACATGTTTCATCGCTGGCTGTGCTCTTTCATCATCAGCACCTCGGCC 420

301 CGCACCATCTACACATGTTTCATCGCTGGCTGTGCTCTTTCATCATCAGCACCTCGGCC 360

301 CGCACCATCTACACATGTTTCATCGCTGGCTGTGCTCTTTCATCATCAGCACCTCGGCC 360

421 ATCGACTTCATTTGATGAGGCGAGGCTCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 480

421 ATCGACTTCATTTGATGAGGCGAGGCTCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 480

361 ATCGACTTCATTTGATGAGGCGAGGCTCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 420

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481 GGACAGCTGCCATTTGGCGCTGGTGACCTGGTGCCCATGTTTCTGTCCACCTGTTGGCG 540

481 GGACAGCTGCCATTTGGCGCTGGTGACCTGGTGCCCATGTTTCTGTCCACCTGTTGGCG 540

421 GGACAGCTGCCATTTGGCGCTGGTGACCTGGTGCCCATGTTTCTGTCCACCTGTTGGCG 480

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481 CCGTACCAGGCCCTTACGCTGTGGGCGAGGGGACCTTGGAGCGAGCGAGCGGCTAGGC 540

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661 GAGCATCAGCTCCCGCGGCTCCGCTGTGCTGCTTTCGAGCAGGTTAGTTCCTG 720

661 GAGCATCAGCTCCCGCGGCTCCGCTGTGCTGCTTTCGAGCAGGTTAGTTCCTG 720

601 GAGCATCAGCTCCCGCGGCTCCGCTGTGCTGCTTTCGAGCAGGTTAGTTCCTG 660

601 GAGCATCAGCTCCCGCGGCTCCGCTGTGCTGCTTTCGAGCAGGTTAGTTCCTG 660

721 ATGAAAGCTACTCTTCTCTGAGAGGCTGTGCTGGGATCTTCTGTCGACAGAGGT 780

721 ATGAAAGCTACTCTTCTCTGAGAGGCTGTGCTGGGATCTTCTGTCGACAGAGGT 780

661 ATGAAAGCTACTCTTCTCTGAGAGGCTGTGCTGGGATCTTCTGTCGACAGAGGT 720

661 ATGAAAGCTACTCTTCTCTGAGAGGCTGTGCTGGGATCTTCTGTCGACAGAGGT 720

781 GAGGGGATCAGGCGCCCGCCAGTTTCTCCAGCTACTCTTACTTCTTCTGCCCCAACACT 840

781 GAGGGGATCAGGCGCCCGCCAGTTTCTCCAGCTACTCTTACTTCTTCTGCCCCAACACT 840

721 GAGGGGATCAGGCGCCCGCCAGTTTCTCCAGCTACTCTTACTTCTTCTGCCCCAACACT 780

721 GAGGGGATCAGGCGCCCGCCAGTTTCTCCAGCTACTCTTACTTCTTCTGCCCCAACACT 780

841 ATCTACAGGAGGACTTACCTTAGGACGCCCTATGTCAGGTGGATTTATGCGCCAAAGAC 900

841 ATCTACAGGAGGACTTACCTTAGGACGCCCTATGTCAGGTGGATTTATGCGCCAAAGAC 900

781 ATCTACAGGAGGACTTACCTTAGGACGCCCTATGTCAGGTGGATTTATGCGCCAAAGAC 840

781 ATCTACAGGAGGACTTACCTTAGGACGCCCTATGTCAGGTGGATTTATGCGCCAAAGAC 840

901 TTTGCCAGCGCCCTGGGATGTGCTCTATGCTCTGCTTCTATCTTCTGCGCGGCTCTGTGTT 960

901 TTTGCCAGCGCCCTGGGATGTGCTCTATGCTCTGCTTCTATCTTCTGCGCGGCTCTGTGTT 960

841 TTTGCCAGCGCCCTGGGATGTGCTCTATGCTCTGCTTCTATCTTCTGCGCGGCTCTGTGTT 900

841 TTTGCCAGCGCCCTGGGATGTGCTCTATGCTCTGCTTCTATCTTCTGCGCGGCTCTGTGTT 900

961 CTGTCTTTTGGCCAAACATGAGCGGAGAGCCCTTTCAGCACCCGCTTTCAGCACCCGCTGCTCTATC 1020

961 CTGTCTTTTGGCCAAACATGAGCGGAGAGCCCTTTCAGCACCCGCTTTCAGCACCCGCTGCTCTATC 1020

901 CTGTCTTTTGGCCAAACATGAGCGGAGAGCCCTTTCAGCACCCGCTTTCAGCACCCGCTGCTCTATC 960

901 CTGTCTTTTGGCCAAACATGAGCGGAGAGCCCTTTCAGCACCCGCTTTCAGCACCCGCTGCTCTATC 960

1021 CTGCATGCCAGCTGGCCAGGCATCTTCATGCTGCTGCTCATCTCTTTGGCTTCTCCAT 1080

1021 CTGCATGCCAGCTGGCCAGGCATCTTCATGCTGCTGCTCATCTCTTTGGCTTCTCCAT 1080

961 CTGCATGCCAGCTGGCCAGGCATCTTCATGCTGCTGCTCATCTCTTTGGCTTCTCCAT 1020

961 CTGCATGCCAGCTGGCCAGGCATCTTCATGCTGCTGCTCATCTCTTTGGCTTCTCCAT 1020

1081 TGCTGGCTCAACGCTTTGGCCAGATGCTACGATTTGGAGACAGAGTGTTCACCGGAC 1140

1081 TGCTGGCTCAACGCTTTGGCCAGATGCTACGATTTGGAGACAGAGTGTTCACCGGAC 1140

1021 TGCTGGCTCAACGCTTTGGCCAGATGCTACGATTTGGAGACAGAGTGTTCACCGGAC 1080

1021 TGCTGGCTCAACGCTTTGGCCAGATGCTACGATTTGGAGACAGAGTGTTCACCGGAC 1080

1141 TGTGGAACTCAACGCTCTTCTCAACTACTACCGCATTTGGAACGTTGGTGGTCCATGAC 1200

1141 TGTGGAACTCAACGCTCTTCTCAACTACTACCGCATTTGGAACGTTGGTGGTCCATGAC 1200

1081 TGTGGAACTCAACGCTCTTCTCAACTACTACCGCATTTGGAACGTTGGTGGTCCATGAC 1140

1081 TGTGGAACTCAACGCTCTTCTCAACTACTACCGCATTTGGAACGTTGGTGGTCCATGAC 1140

1201 TGCTGTGTACAGCTACGCTGTATCAGGATGGGCTGGGCTCTTGGTGGGCGGCGGAGG 1260

1201 TGCTGTGTACAGCTACGCTGTATCAGGATGGGCTGGGCTCTTGGTGGGCGGCGGAGG 1260

1141 TGCTGTGTACAGCTACGCTGTATCAGGATGGGCTGGGCTCTTGGTGGGCGGCGGAGG 1200

1141 TGCTGTGTACAGCTACGCTGTATCAGGATGGGCTGGGCTCTTGGTGGGCGGCGGAGG 1200

1261 GTAGCCATGCTGGGTGTCTCCGAGTGGCCCATGAGTATATCTTCTGCTTC 1320

1261 GTAGCCATGCTGGGTGTCTCCGAGTGGCCCATGAGTATATCTTCTGCTTC 1320

1201 GTAGCCATGCTGGGTGTCTCCGAGTGGCCCATGAGTATATCTTCTGCTTC 1260

1201 GTAGCCATGCTGGGTGTCTCCGAGTGGCCCATGAGTATATCTTCTGCTTC 1260

1321 GTCTGGGGTCTTCTTCTATCCCGTATGCTGATATCTTCTTGTGATGGAGGAATGTG 1380

1321 GTCTGGGGTCTTCTTCTATCCCGTATGCTGATATCTTCTTGTGATGGAGGAATGTG 1380

Db 1261 GTCTGGGTTCTATCCCGTCATGCTGATCTTCTCTCATGAGAAATGTTG 1320  
 QY 1381 AACTTCATGATGATGACACGACCGCGCCCGCATGGAACGCTGCTGATGTGGACCATG 1440  
 Db 1321 AACTTCATGATGATGACACGACCGCGCCCGCATGGAACGCTGCTGATGTGGACCATG 1380  
 QY 1441 CTGTTTCTAGGCGAGGAAATCCAGTTCAGCTCTACTGCCAGAGTGGTACGACACGGCGG 1500  
 Db 1381 CTGTTTCTAGGCGAGGAAATCCAGTTCAGCTCTACTGCCAGAGTGGTACGACACGGCGG 1440  
 QY 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGTGTGACACCTCGACTTGGTCTGCTGC 1560  
 Db 1441 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGTGTGACACCTCGACTTGGTCTGCTGC 1500  
 QY 1561 CATACTAG 1569  
 Db 1501 CATACTAG 1509

## RESULT 3

AAZ57359  
ID AAZ57359 standard; cDNA; 1607 BP.

AC AAZ57359;

XX  
XX  
DT 05-APR-2000 (first entry)

DE Mouse acyl CoA:cholesterol acyltransferase 2 encoding cDNA.

XX Mouse; acyl CoA:cholesterol acyltransferase; ACAT-2; diagnosis;  
 KW antilipemic; hypercholesterolaemia; hypertriglyceridaemia;  
 KW hyperlipidaemia; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FT CDS 30..1607

FT /\*tag= a

FT /product= "ACAT-2"

XX W09967368-A1.

XX 29-DEC-1999.

XX 16-JUN-1999; 99WO-US13683.

XX 23-JUN-1998; 98US-0090354.

XX 08-JUN-1999; 99US-0328857.

XX (REGC ) UNIV CALIFORNIA.

PA Cases S, Farese RV, Novak S, Erickson SK;

XX WPI; 2000-106291/09.

XX P-PSDB; AA67952.

XX Novel polypeptide, useful to treat conditions associated with elevated

XX cholesterol ester levels e.g. hypercholesterolemia

XX Example; Page 51; 57pp; English.

XX The present sequence encodes the mouse acyl CoA:cholesterol

XX acyltransferase designated ACAT-2. ACAT-2 polypeptides can be

XX administered therapeutically, especially by expressing encoding

XX polynucleotides, to treat individuals in need of ACAT-2 polypeptide.

XX They may especially be administered to treat disease conditions

XX associated with elevated cholesterol ester levels e.g.

XX hypercholesterolaemia or hyperlipidaemia (including

XX hypertriglyceridaemia), since ACAT-2 catalyses the esterification of

XX cholesterol with fatty acyl CoA substrates. The polypeptides can also

XX be used to diagnose diseases related to polypeptide expression or

XX activity, by analysing for polypeptide presence or amount in a sample.

CC They are useful to screen for compounds inhibiting or activating the  
 CC polypeptide, which can be included in pharmaceutical compositions and  
 CC administered therapeutically to treat conditions associated with ACAT-2;  
 CC inhibitory agents can especially be used to inhibit ACAT-2 activity;  
 CC especially therapeutically, and especially agents which selectively  
 CC inhibit ACAT-2 and not prior art ACAT-1.  
 XX  
 SQ Sequence 1607 BP; 299 A; 466 C; 456 G; 385 T; 1 other;

Query Match 70.9%; Score 1112.4; DB 21; Length 1607;  
 Best Local Similarity 83.2%; Pred. No. 3.7e-267;  
 Matches 1295; Conservative 0; Mismatches 247; Indels 15; Gaps 2;

QY 28 CTCGAGGACAGACAGAGGCTGGGAGGAGCGGACGCAACCCCTGT---GCAGATGA 84  
 Db 51 CTTGGGAGGAGAGAGGGCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGG 110  
 QY 85 AACACTGACAGCAGACAGAGCCCGGACTTGGTACAATGACCCGACACATGAGGCTGTG 144  
 Db 111 AACGCAAGGACACACCGAAACCCGACACTTGGTGCATGACATGAGGCTGTG 170  
 QY 145 AAGGCACAATTGCTGGAGCAAGCGCAGGAGGACAACTGAGGAGCTGCTGATCGGGCATG 204  
 Db 171 AGACNCAGTTTCTGGAGCAAGCAGAGAGAGTGGCAGAGCTGTGATCGGGCCCTA 230  
 QY 205 CGGGAGGCTATACAATCTCTACCCATCACAGACAAACCTCTGCCCCACCTCCCCAGGT 264  
 Db 231 TGGGAGGCTATCAAGCTTACCCCAACAAAGACAGACCTCTTCCCTCCGCTGCCAGAT 290  
 QY 265 TCTTGGAGCAGCAGCAGGAGCCATCCCTGGGGAACAGAAAGTTTCAATATCCGCAAG 324  
 Db 291 TCTACAAGCAAGACCCCGGAGTTACGCCCTGGAAAACGGAAAAGTTTCTGCTCCGCGCAAG 350  
 QY 325 TCCCTGCTGATGAGCTGATGAGGTGACAGCATTTCCGACCATCTACCACATGTTTCATC 384  
 Db 351 TCACGTGATGATGAGCTATGAGGAGTGCAACATTTCCGAAACCATCTACCACATGTTTCATC 410  
 QY 385 GCTGGCTGTGTCTTTCATCATCAGCACCCCTGGCCATCGACTTTCATGATGAGGCGAG 444  
 Db 411 GCGGGCTATGTTCTTGTATCATCAGCACCCCTGGCCATCGACTTTCATGATGAGGCGAG 470  
 QY 445 CTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTCGGCGCTGGTG 504  
 Db 471 TTGATGCTGGAGTTTGACTTACTCTTTCAGCTTCGGACAGCTGCCCTTCGCGTGTAGT 530  
 QY 505 ACCTGGGTGCCCATGTTTCTGTCCACCCCTGTTGGCGCGCTACAGGCCCTACGCTGTGG 564  
 Db 531 ACCTGGGTGCCCATGTTTCTGTATAGCTCTCTAGTGGCTTACACACCTGTGGCTGTGG 590  
 QY 565 GCCA-----GGGGCACCTGGAGCAGCGCGGCGCTGGGCTGTGCGCTTTTA 612  
 Db 591 GCGAGGCGCGCGCTGGGGGTGCTTGGATGCTGGGGCGCAGCTGGGCTGCTTCTGCTG 650  
 QY 613 GCGGCGCAGCGGTGCTGCTGCGCGCTGCGGCTCCAGTGGCGCTGGAGCATCAGCTC 672  
 Db 651 GCTGCCACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710  
 QY 673 CGCGCGGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732  
 Db 711 CGCGCGGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770  
 QY 733 TCTTCTCTGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792  
 Db 771 TCTTCTCTGAGAGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830  
 QY 793 GCCCGCAGTTTCTCCAGCTACTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 852  
 Db 831 CCCCCAAGTTTCTCCAGCTACTCTACT 890  
 QY 853 ACTTACCTAGGACCCCTATGTGAGTGGAAATTTATGTGGCAAGAACTTTGCCCGAGGCC 912  
 Db 891 ACATACCCCGCAGCACCCAGCATCAGGTGGAATATGTGGCAAGAACTTTGCCCGAGGCC 950



QY 1441 CTGTTTCTAGCCAGGAATCCAGGTACGCTGTACTGCCAGGAGTGGTACGACGGGG 1500  
 DB 544 CTGTTTCTAGCCAGGAATCCAGGTACGCTGTACTGCCAGGAGTGGTACGACGGGG 603  
 QY 1501 CACTGCCCTTACCCAGGCACTTCTGGGGCTGGTGACACCTCGATCTTGGTCTGCG 1560  
 DB 604 CACTGCCCTTACCCAGGCACTTCTGGGGCTGGTGACACCTCGATCTTGGTCTGCG 663  
 QY 1561 CATACCTAG 1569  
 DB 664 CATACCTAG 672

RESULT 5  
 ID AAQ63212 standard; cDNA; 4011 BP.  
 AC AAQ63212;  
 XX  
 DT 03-JAN-1995 (first entry)  
 DE Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).  
 XX  
 KW Acetyl coenzyme A: cholesterol acetyltransferase; ACAT; disease;  
 KW diagnosis; detection; screening; treatment; prophylaxis;  
 KW hypercholesterolaemia; atherosclerosis; antisense; probe;  
 KW identification; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT 1397..3049  
 FT CDS  
 FT /tag= a  
 FT /product= Acetyl CoA: cholesterol acetyltransferase  
 FT polyA\_signal  
 FT 3385..3389  
 FT /tag= b  
 FT /note= "Putative polyadenylation signal."  
 FT polyA\_signal  
 FT 3962..3967  
 FT /tag= c  
 FT /note= "Putative polyadenylation signal."  
 XX  
 XX WO9409126-A.  
 XX  
 XX 28-APR-1994.  
 XX  
 XX 12-OCT-1993; 93WO-US09704.  
 XX  
 XX 14-OCT-1992; 92US-0959950.  
 XX  
 XX 10-SEP-1993; 93US-0121057.  
 XX  
 XX (DART-) DARTMOUTH COLLEGE.  
 XX  
 XX Chang CCY, Chang T;  
 XX  
 XX WPI; 1994-151312/18.  
 DR P-PSDB; AAR53079.  
 XX  
 XX Acetyl coenzyme A: cholesterol acetyl-transferase and nucleic  
 PT acid sequence encoding it - used to correct enzyme deficiencies  
 PT and screen for enzyme inhibitors  
 XX  
 XX Claim 13; Figure 9; 52pp; English.  
 XX  
 XX The acetyl coenzyme A: cholesterol acetyl-transferase (ACAT) gene  
 CC sequence enables the screening of human populations for abnormal  
 CC human ACAT activities for disease diagnosis. It provides  
 CC information concerning the catalytic mechanism of ACAT and allows  
 CC the design of drugs serving as specific ACAT inhibitors, desirable  
 CC for the prevention and/or treatment of human hypercholesterolaemia  
 CC and human atherosclerosis. It also allows the design of antisense  
 CC DNAs or RNAs to inhibit ACAT production, or probes to identify  
 CC different forms of human ACAT or ACAT from different animal species.

CC This sequence is a human ACAT cDNA sequence designated K1.  
 XX  
 SQ Sequence 4011 BP; 1056 A; 793 C; 839 G; 1323 T; 0 other;  
 Query Match 26.0%; Score 407.2; DB 15; Length 4011;  
 Best Local Similarity 59.0%; Pred. No. 2.8e-91;  
 Matches 768; Conservative 0; Mismatches 508; Indels 26; Gaps 3;  
 QY 287 CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGATGATGATGG 346  
 DB 1737 CACCTCCAGAACAGAAAGATTTTATTTGCAAGCGCTCTCTCTAGTAGAAGTGTG 1796  
 QY 347 AGGTGACAGATTTCGACCATCTACACATGTTTCATCGTGGCCCTGTGTGTTTCATCA 406  
 DB 1797 AAGTGGACCATCAGAACATATATACATGTTTATTGGCCCTCCTATCTCTTTATCC 1856  
 QY 407 TCAGCACCCCTGGCCATCGACTTCATTGATGAGGGCAGGCTGCTGCTGGATTTGACCTAC 466  
 DB 1857 TCAGCACACTTGTAGTAGATTACATTGATGAAGGAAGGCTGGTGTGAGTTTCAGCCCTC 1916  
 QY 467 TGATCTTCAGTTTCGACAGCTGCCATTGGCGCTGGTGGCTGGTGGTGGTGGTGGTGGT 526  
 DB 1917 TGTCTTATCTTTTGGCAAAATTTCTACCGTGTGTTGGACCTGGTGGATCATGTTCTGT 1976  
 QY 527 CCACCTGTGGCGCGGTACAGGCCCTACGGCTGTGGCCAGGGGACCTGGAGCAGG 586  
 DB 1977 CTACATTTTTCAGTCCCTATTTCTGTTTCAACATTTGGCGCACTGGCTATAGCAAGATT 2036  
 QY 587 CGACGGGCTGGCTGTGGCTTTTAGCGGCCACCGCTGGTGGTGGTGGTGGTGGTGGTGG 646  
 DB 2037 CTCATCCGCTGATCCGTTCTCTTCCATGGCTTTCTTTTCAATGATTTCCAGATTGGAG 2096  
 QY 647 TCC-----ACGTGGCGGTGGAGCATCAGCTCCCGCGGCTCCCGT 688  
 DB 2097 TTCTAGTTTGGACCAACATATGTTGTTAGCATATACACTGCCACAGCTTCCCGGT 2156  
 QY 689 GTGCTCTGTTCGACGAGGTAGTTCCTGATGAAGAGTACTCTCTCTCTGAGAGAGG 748  
 DB 2157 TCATCATTTATTCGACGAGATTCTGTTTGAATGAAGGCCCACTCATTTGTGACAGAGA 2216  
 QY 749 CTGCTCTGGGATCTTCGTGCCAGAGGTGAGGGGATCCAGGCCCGCCAGTTTCTCCA 808  
 DB 2217 ACGTGCCTGGGTACTAAAT-TCAGCTAAGAGAAATCAAGCACTGTTCATATAGCTACA 2275  
 QY 809 G-----CTACCTCTACTTCTCTTCTGCCAACACTATCTACAGGAGACTTACCT 861  
 DB 2276 GTCAACCACTATTGTACTTCTTATTTGCTCTACCTTATCTACCGTGACAGTACCC 2335  
 QY 862 AGGAGCCCTATGTCAGTGGAAATATGTGGCCAAAGAACTTTGCCAGGCCCTGGGATCT 921  
 DB 2336 AGGAATCCCACTGTAAGATGGGGTTATGTCGTATGAAGTTTGCACAGCTCTTTGGTGC 2395  
 QY 922 GTGCTCTATGCTGCTTCATCTCGGCCCGCTCTGTGTCTCTCTTTGCCAACATGAGC 981  
 DB 2396 TTTTCTATGTACTACATCTTTGAAGGCTTTGGCCCGCTTTGTCGGAATCAAA 2455  
 QY 982 CGAGAGCCCTTCAGCACCCGTCGCTGTGTCTCTATCTGATGCCACGTTGCCAGGC 1041  
 DB 2456 CAGGAGCCCTTCAGGCGCTGCTGTCTGTGCTCTATGTTTAACTCCATCTTGGCAGGT 2515  
 QY 1042 ATCTTCATGCTGCTGCTCATCTTCTTGGCTTCTCCCTGCTGCTGCTCAAGCCCTTGGC 1101  
 DB 2516 GTGCTGATTTCTTCTTACTTTTGGCTTTTGGCTGCTGCTGCTCAATGCCCTTGTCT 2575  
 QY 1102 GAGATGCTACGATTTGGAGACAGGATGTTCTACCGGAGCTGGTGGAACTCAACGCTCTTC 1161  
 DB 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAGAGATTGGTGGAACTCCAGCTATAC 2635  
 QY 1162 TCCAACTACTACCGCACTTTGGAACGTTGGTGGTCCATGACTGGCTGTACAGTACGTGTAT 1221  
 DB 2636 TCCAACTATTATAGAACCTGGAATGTGGTGGTCCACTGACTGGCTATATTACTATGCTTAC 2695  
 QY 1222 CAGGATGGGCTGGGCTCTCTTGGTGGCCCGGCCGAGGGGTAGCCATGCTGGTGTGTTTC 1281







Db 2576 TGAGATGTTACGCTTTGGTGACAGGATGTTCTATAGGANTGGTGAACCTCCAGTGCATA 2635  
QY 1161 CTCACACTACTACGCACTTGGAACTGGTGTCCATGACCTGCTGTACAGCTACGCTGA 1220  
Db 2636 CTCACACTATTTAGAACCTGGAATGGTGTCCATGACCTGCTGTATTTACTATGCTTA 2695  
QY 1221 TCAGGATGGGTGGCGCTCTCTGTTGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTT 1280  
Db 2696 CAAGGACTTTCTCTGGTTTTCTCCAAGAGATTCAAAATCTGCTGCCATGTTAGCTGCTT 2755  
QY 1281 CCTGGTCTCCGAGTGGCCGATGATATATCTTCTGCTTCTGCTGGGTCTTCTATACC 1340  
Db 2756 TCGTGTATCTCTAGTACAGGAATGCTTGGCTTGGTGTGCTGCTGCTTCTTCTATCC 2815  
QY 1341 CGTCATGCTGATCTCTCTCTGTCATTGGAGGAATGTTGAATTCATGATGATGACCA 1400  
Db 2816 CGTCTGTTCTGCTCTCTCTGTTCTTGGAAATGGCTTCACTTCATGTCATGATAG 2875  
QY 1401 GCGACCGGCGCCGATGGAACGCTGCTGATGTGGACCATGCTGTTCTAGCCAGGGAAT 1460  
Db 2876 TCGGAAAAAGCCGATTTGGAATGCTGATGTGGACTTCTCTTTTCTTGGCAATGGAGT 2935  
QY 1461 CCAGGTCAGCTGTACTGCCAGGAGTGTACGACGCGGGGACCTGCCCCCTTACCCAGGC 1520  
Db 2936 CTTACTCTGCTTTTATCTCAAGAAATGGTATGACGCTGGGCACTGCTCTCGAAAAATCC 2995  
QY 1521 AACTTTCTGGGGGCTGGTGACACCTCGATCTTGGTCTGCGCAT 1563  
Db 2996 CACATTTTGGATATGTCGGGCCACGTTCTGAGACTTGCTGT 3038

RESULT 8  
AAV01545  
ID AAV01545 standard; DNA; 455 BP.  
AC AAV01545;  
XX  
XX  
DT 08-JUN-1998 (first entry)  
XX  
DE Acylcoenzyme A:cholesterol acyltransferase partial sequence.  
XX  
KW Acylcoenzyme A:cholesterol acyltransferase; ARGP-1; ARGP-2;  
KW ACAT related gene product; sterol esterification;  
KW inhibitor; atherosclerosis; hyperlipidaemia; ss.  
XX  
OS  
XX  
XX  
Key Location/Qualifiers  
FT CDS 1..195  
FT /\*tag= a  
XX W09745439-A1.  
XX  
PD 04-DEC-1997.  
XX  
XX 30-MAY-1997; 97WO-US09460.  
XX  
XX 30-MAY-1996; 96US-0657620.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX Sturley SL;  
XX  
XX WPI: 1998-032573/03.  
XX P-PSDB; AAW43413.  
XX  
XX DNA encoding acylcoenzyme A: cholesterol acyltransferase II or  
XX III - useful to identify inhibitors for treatment of  
XX atherosclerosis or hyperlipidaemia  
XX  
XX Disclosure; Page 70; 121pp; English.  
XX  
XX This is a nucleic acid sequence of the invention. The invention

CC relates to isolated nucleic acids (see AAV01533-35) coding for human  
CC and mouse acylcoenzyme A:cholesterol acyltransferase II and III (see  
CC AAW43406-08), also designated ACAT related gene products (ARGP) 1  
CC and 2. These can be used to identify inhibitors useful in the  
CC treatment of atherosclerosis and hyperlipidaemia.  
XX  
SQ Sequence 455 BP; 95 A; 121 C; 123 G; 116 T; 0 other;  
Query Match 12.2%; Score 191.8; DB 19; Length 455;  
Best Local Similarity 99.0%; Pred No. 5.8e-38;  
Matches 193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1375 ATGTTGAACCTTCATGATGATGACGACGCGGCGGATGACGCTGCTGATGTTGG 1434  
Db 1 ATGTTGAACCTTCATGATGATGACGACGCGGCGGATGACGCTGCTGATGTTGG 60  
QY 1435 ACCATGCTGTTTCTAGGCCAGGGAATCCAGTCCAGCTGCTACTGCCAGGAGTGGTACCA 1494  
Db 61 ACCATGCTGTTTCTAGGCCAGGGAATCCAGTCCAGCTGCTACTGCCAGGAGTGGTACCA 120  
QY 1495 CGCGGCGACTGCCCTTACCCAGGCAACTTCTTGGGGGCTGGTGACACCTCGATCTTGG 1554  
Db 121 CGGAGCGACTGCCCTTACCCAGGCAACTTCTTGGGGGCTGGTGACACCTCGATCTTGG 180  
QY 1555 TCCTGCCATACCTAG 1569  
Db 181 TCCTGCCATACCTAG 195  
RESULT 9  
ABL13759  
ID ABL13759 standard; cDNA; 1885 BP.  
XX  
AC ABL13759;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 35759.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN W0200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US09231.  
XX  
XX 23-MAR-2000; 2000US-191637P.  
XX 11-JUL-2000; 2000US-0614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI: 2001-656860/75.  
XX P-PSDB; ABB69656.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from Drosophila and for elucidating cell signalling and cell-cell  
XX interactions -  
XX  
XX Claim 1; SEQ ID NO 35759; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
XX useful in developmental biology and in elucidating cell signalling and  
XX cell-cell interactions in higher eukaryotes for the development of  
XX insecticides, therapeutics and pharmaceutical drugs. The invention  
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
XX sequences (ABL01840-ABL16175) and the encoded proteins

CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1885 BP; 410 A; 514 C; 504 G; 457 T; 0 other;  
  
Query Match 11.0%; Score 172; DB 23; Length 1885;  
Best Local Similarity 51.9%; Pred. No. 8.5e-33;  
Matches 413; Conservative 0; Mismatches 380; Indels 3; Gaps 1;  
  
QY 774 ACGAGTGTAGGGATCCAGGCCCCAGTTTCTCCAGCTACTCTCTCTCTCTGCCC 833  
D 1001 AGGCAGTGTAGGACCCCTTTGTGCGCGCTGAGCTTTACAGCTACTTTTGTGTCAC 1060  
QY 834 AACACTCATCTACAGGAGACTTACCTAGGAGCCCTATGCTCAGGTGGAATTTATGCG 893  
D 1061 CAGCTTATCTACGAGACAGTACCCGCGCACCTCCACATCCGCTGGAATTTGCCCT 1120  
QY 894 CAAGAACTTTGCCAGGCCCTGGGATGTGTCTCTATGCTCTCTCTCTCTCTGCGCCCT 953  
D 1121 GAATCAGCTGTGTGGAGTGTGGCCATAGCTTCTCTGTACGGTTTCATCATGAGCGCA 1180  
QY 954 CTGTGTCTCTGTCTTGTCCCAACATAGCCGAGAGCCCTTCAGCACCCCTGCGCTGTGCT 1013  
D 1181 CATCCAGGACACTTCGGACAGTACGAGCTGGAACCAATGGGACCTCCAGCTGATCCT 1240  
QY 1014 CTCTATCTCTGATGCCACGTTGCCAGGCATCTTCTATGCTGCTCTCTCTCTCTCTCT 1073  
D 1241 CAAGCTGTTCGGCATGATGCTGCCAGCGGGTGATCTTCTGTGCGGCTTCTACCTAAT 1300  
QY 1074 CTCTATCTCTGCTCAAGCCCTTTCCGAGATGTACAGATTTGGAGACAGGATGTTCTA 1133  
D 1301 CTGTCACTCTGTGCTGAACTTACGTCGGAGCTGTACGCTTGGTGATCGAATGTTCTA 1360  
QY 1134 CCGGGAGTGTGGAACCTCAACGCTCTTCCAACTACTACCGACACTTGAAGCTGTGCT 1193  
D 1361 CAAGGACTGTGTGAGCTGCGACACTTACGATGCTCTACGAAACTGGAATGTCTGCTGT 1420  
QY 1194 CATGACTGTCTACAGCTACGTGTATCAGGATGGGCTGCGGCTCTCTGCTGCGCGGG 1253  
D 1421 GCACGACTGTCTACGAGTACGTGTACAGGATATGTACACTCATGTGTCCGAGGTTT 1480  
QY 1254 CCGAGGGTGTAGCATGCTGGGTGTCTCTGCTCCGAGTGGCCCATGATATATCTT 1313  
D 1481 CAAGGTGGCGGCTCGCTGSCAGTGTTCATGATCTCCGCTGTGCTGATGAGCAGGTTCT 1540  
QY 1314 CTGCTTCTGCTGGGTTCTCTCTATCCGCTCATGCTGATCTCTCTCTCTCTCTCTCT 1373  
D 1541 CGCTTTGCTGCTCAAAATGTTCTCCAGTGTGTTCTCTCTCTCTCTCTCTCTCTCTCT 1600  
QY 1374 AATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1433  
D 1601 TGCTTTGGTATCTTAATGGGAGTCTCCAAAGATGATG---GCAACATCTTCTCTGT 1657  
QY 1434 GACCATGCTGTGTTTCTAGGCGAGGAATCCAGGTACGCTGTACTGCGAGAGTGTACGC 1493  
D 1658 GTTCTCTGATCTCTGGGAAATGCCAGCTGTATCTCACTATACGCCATGAGCATTAACG 1717  
QY 1494 ACGGCGGACCTGCCCCCTTACCCAGGCACTTCTCTGGGGGCTGTTGACACCTCGATCT 1553  
D 1718 CTTAAGAACTGCAACCTTAAGCAACAGAGATTGGAGTATGCTGCTCTCTCTCTCTCT 1777  
QY 1554 GTCTTGCCTATACCTAG 1569  
D 1778 GCCTCTGCTACATTAAG 1793  
  
RESULT 10  
ID ABL15694  
XX ABL15694 standard; cDNA; 2657 BP.  
AC ABL15694;

XX  
DT 26-MAR-2002 (first entry)  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41564.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
XX  
PT P-PSDB; ABB71591.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
XX interactions  
XX  
PS Claim 1; SEQ ID NO 41564; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA  
CC sequences (AB101840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 2657 BP; 704 A; 610 C; 624 G; 719 T; 0 other;  
  
Query Match 11.0%; Score 172; DB 23; Length 2657;  
Best Local Similarity 51.9%; Pred. No. 9.6e-33;  
Matches 413; Conservative 0; Mismatches 380; Indels 3; Gaps 1;  
  
QY 774 ACGAGTGTAGGGATCCAGGCCCCAGTTTCTCCAGCTACTCTCTCTCTCTGCCC 833  
D 185 AGGCAGTGTAGGACCCCTTTGTGCGCGCTGAGCTTTACAGCTACTTTTGTGTCACC 244  
QY 834 AACACTCATCTACAGGAGACTTACCTAGGAGCCCTATGCTCAGGTGGAATTTATGCG 893  
D 245 CAGCTTATCTACGAGACAGTACCCGCGCACCTCCACATCCGCTGGAATTTGCCCT 304  
QY 894 CAAGAACTTTGCCAGGCCCTGGGATGTGTCTCTATGCTCTCTCTCTCTCTGCGCCCT 953  
D 305 GAATCAGCTGTGTGGAGTGTGTGGCCATAGCTTCTCTGTACGGCTTTCATCATGAGCGGA 364  
QY 954 CTGTGTCTCTGTCTTGTCCCAACATGAGCGGAGAGCCCTTCAGCACCCGCTGCTGTGCT 1013  
D 365 CATCCAGGACACTTCGGACAGTACGAGCTGGAACCAATGGGACCTCCAGCTGATCCT 424  
QY 1014 CTCTATCTCTGATGCGACCTGTGCGAGGATCTTCTATGCTGTGCTCATCTCTTCCCTT 1073  
D 425 CAAGCTGTTCGGCATGATGCTGCCAGCGGTGATCTTCTGTGCGGCTTCTACCTAAT 484  
QY 1074 CTCTCATCTGCTGGCTCAAGCCCTTTGCCAGATGCTTACCATTTGGAGACAGGATGTTCTA 1133  
D 485 CCTGCACCTGCTGGCTGAACTTACGTCGGAGCTGTACGCTTCCGCTGATCGAATGTTCTA 544



## RESULT 12

AAQ63210  
 ID AAQ63210 standard; cdNA; 996 BP.  
 AC  
 AC AAQ63210;  
 XX  
 DT 03-JAN-1995 (first entry)  
 XX  
 DE Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).  
 XX  
 KW Acetyl coenzyme A; cholesterol acetyltransferase; ACAT; disease;  
 KW diagnosis: detection; screening; treatment; prophylaxis;  
 KW hypercholesterolaemia; atherosclerosis; antisense; probe;  
 KW identification; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO9409126-A.  
 XX  
 XX 28-APR-1994.  
 XX  
 XX 12-OCT-1993; 93WO-0509704.  
 PF  
 XX 14-OCT-1992; 92US-0959950.  
 PR 10-SEP-1993; 93US-0121057.  
 XX  
 PA (DART-) DARTMOUTH COLLEGE.  
 XX  
 XX Chang CCY, Chang T;  
 XX  
 XX WPI; 1994-151312/18.  
 DR  
 XX  
 XX Acetyl coenzyme A: cholesterol acetyl-transferase and nucleic  
 PT acid sequence encoding it - used to correct enzyme deficiencies  
 PT and screen for enzyme inhibitors  
 XX  
 PS Claim 13; Figure 3; 52pp; English.  
 XX  
 CC The acetyl coenzyme A: cholesterol acetyl-transferase (ACAT) gene  
 CC sequence enables the screening of human populations for abnormal  
 CC human ACAT activities for disease diagnosis. It provides  
 CC information concerning the catalytic mechanism of ACAT and allows  
 CC the design of drugs serving as specific ACAT inhibitors, desirable  
 CC for the prevention and/or treatment of human hypercholesterolaemia  
 CC and human atherosclerosis. It also allows the design of antisense  
 CC DNAs or RNAs to inhibit ACAT production, or probes to identify  
 CC different forms of human ACAT or ACAT from different animal species.  
 CC This sequence is a human ACAT cDNA clone designated C1.  
 XX  
 XX Sequence 996 BP; 258 A; 219 C; 207 G; 312 T; 0 other;  
 SQ

Query Match 8.6%; Score 134.6; DB 15; Length 996;  
 Best Local Similarity 53.1%; Pred. No. 1.4e-23;  
 Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;

QY 287 CATCCCTGGGGAACAGAAAGTTTCATCATCGCAAGTCCCTGCTGTATGAGCTCATGG 346  
 DB 262 CACCTCCAGAACAAAGAAAGATTTTATTGCAAGCGCTCTCTCTTAGATGAAGTCTG 321  
 QY 347 AGGTGAGCAGATTTCCGCAACCATACACATGTCATCGCTGGCCGTGTGCTTTCATCA 406  
 DB 322 AAGTGGACCACATCAGACAATATACATGTTTATGCCCTCCTCATCTCTTTATCC 381  
 QY 407 TCAGACCCCTGGCCATCGACTTCATGATGAGGGCAGGCTGCTGG--AGTTTGACCT 464  
 DB 382 TCAGCACACTTGTAGTAGATTACATTGATGAAGGAAGGCTGTGCTGCAAGTTACGCC 441  
 QY 465 ACTG-ATCTTCAGTTCGAGACCTGCCATTGGCGGTGGTACCTGGGTGCCCATGTTTC 523  
 DB 442 CCTGTCTTAGCATTTTGGCAATTTCTTACCGTGTGTTGGACCTGGTGGATCATGTTCC 501  
 QY 524 TGTCACCTGTTGGCGCGGTACAGGCCCTACGGCTGTGGGCGAGGGCACCTGGACGC 583

Db 502 TGCTACATTTTCAGTTCCTATTTTCTGTTCAACATTTGGCGCATGGCTATAGCAAGA 561  
 QY 584 AGCGACGGGCGCTGGCTGTGGCTTTTAGCGCGCCACGCGGTGGTCTC----- 633  
 Db 562 GTTCTCATCGCGTATCCGTTCTCTCTTCATGCTTTCTTTTCATGATTTCCAGATTG 621  
 QY 634 ---TGCGCGCTGCCGCTCCACGTTGGCGGTGGAGCATCAGTCCCGCGGCTCCCGTTGT 690  
 Db 622 GAGTTCTAGTTTGGACCAACATATGTTGTTAGCATATCTGCCACCATGTTCCCGG 681  
 QY 691 GTCTGTCTTCAGCAGGTTAGTTCCTTCATGAAAGCTACTCTCTTCCTGAGAGGCT 750  
 Db 682 TTTATCATTTTCGACAGATGCTTTTGTAAATGAAGGCCCATCTATTGTGACAGAGA 741  
 QY 751 GTGCTGGGATCCTTCGTGCCAGCAGGTGAGGGATCCAGGCC-----CCCAGTTTCT 805  
 Db 742 GTGCTCGGTACTAATTCAGCTAAGGAGAAATCAAGCACTGTTCCAATACCTACAGTCA 801  
 QY 806 CCAGCTACCTCTACTTCTCTTCGCCCACACTATCTACAGGAGACTTACCCCTAGGA 865  
 Db 802 ACCAGTATTGTACTTCTTATTTGCTCCTACCTTATCTACCGTGACAGCTATCCAGGA 861  
 QY 866 CGCCTATGTCAGGTGGAATTTATGTCGCAAGAACTTTGCCCAGGCCCTGGGATGTGC 925  
 Db 862 ATCCCACTGTAAGTGGGTTATGTTGCTATGAAGTTTGCACAGGCTTTGGTGTCTTT 921  
 QY 926 TCTATGCTCTGCTTCATCTCGGCGGCTCTGTGTTCTCTGTTTGGCAACATCAGCGGAG 985  
 Db 922 TCTATGTTACTACTATCTTTGAAAGGCTTTGTGCCCCCTGTTTCGGAATATCAACAGG 981  
 QY 986 AGCCCTTCAGACCC 1000  
 Db 982 AGCCCTTCAGCGCTC 996

RESULT 13  
 AA01539  
 ID AA01539 standard; cdNA; 983 BP.  
 XX  
 AC AA01539;  
 XX  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Human acylcoenzyme A:cholesterol acyltransferase II (ACAT-II), DNA.  
 XX  
 KW Acylcoenzyme A:cholesterol acyltransferase; ACAT I;  
 KW ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;  
 KW inhibitor; atherosclerosis; hyperlipidaemia; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..660  
 FT /\*tag= a  
 PN WO9745439-A1.  
 XX  
 PD 04-DEC-1997.  
 XX  
 XX 30-MAY-1997; 97WO-US09460.  
 XX  
 XX 30-MAY-1996; 96US-0657620.  
 PR (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA Sturley SL;  
 XX  
 DR WPI; 1998-032573/03.  
 DR P-PSDB; AAW43412.  
 XX  
 PT DNA encoding acylcoenzyme A: cholesterol acyltransferase II or  
 PT III - useful to identify inhibitors for treatment of  
 PT atherosclerosis or hyperlipidaemia

XX Disclosure; Page 68; 121pp; English.

XX This nucleic acid molecule encodes human acylcoenzyme A:cholesterol

CC acyltransferase I (see AAW43412), or ACAT II. The invention relates

CC to isolated nucleic acids (see AAW01533-35) coding for human and

CC mouse acylcoenzyme A:cholesterol acyltransferase II and III (see

CC AAW43406-08), also designated ACAT related gene products (ARGP) 1

CC and 2. These can be used to identify inhibitors useful in the

CC treatment of atherosclerosis and hyperlipidaemia.

XX

SQ Sequence 983 BP; 193 A; 314 C; 263 G; 213 T; 0 other;

Query Match 6.1%; Score 95; DB 19; Length 983;

Best Local Similarity 58.7%; Pred. No. 1e-13;

Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCTGTCATGCCAGTGGCCAGGATCTTCATGCTGCTCATCTTCTTTCCTTCCTCC 1078

DB 182 TCTGAAGCTGGCGGTCCCAATCAGCTCATCTGGCTCATCTTCTTACTGGCTCTTC 241

QY 1079 ATTGCTGGCTCAAGCTTTGCCAGATGCTACGATTTGGAGACAGATCTTACCGGG 1138

DB 242 ACTCTGCTGGAATGGCGTGGCTGAGCTCATGAGTTGGAGACCGGAGTTCTACCGGG 301

QY 1139 ACTGGTGGAACTCAAGCTCTTCTTCCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198

DB 302 ACTGGTGGAACTCCGAGTCTGTACCTACTTCTGGCAGAACTGGAATCCCTGTGCACA 361

QY 1199 ACTGGCTGTACAGTACGTTATCAGATGGCTGGGCTTCCTTGGTGGCCGCGCCGAG 1258

DB 362 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTGCAC-----GGGGCAGCAGCAAGT 415

QY 1259 GGGTAGCAGCTGGGTGTCTTCTTCCGTCCTCCAGTGGCCCATGATATCTTCTGCT 1318

DB 416 GGATGGCCAGACAGGGGTGTTCTTGGCTCGGCTTTTCCACAGAGTACCTGGTAGCG 475

QY 1319 TCGTCTGGGGTTCCTC 1335

DB 476 TCCCTCTGCGAATGTC 492

RESULT 14

ABA06413/C

ID ABA06413 standard; cDNA; 993 BP.

XX

AC ABA06413;

XX

DT 10-JAN-2002 (first entry)

XX

DE Human cDNA SEQ ID NO: 79.

XX

KW Human; gene therapy; neural disorder; immune system disorder;

KW muscular disorder; reproductive disorder; gastrointestinal disorder;

KW pulmonary disorder; cardiovascular disorder; renal disorder;

KW proliferative disorder; inflammation; ss.

XX

OS Homo sapiens.

XX

PN WO200154474-A2.

XX

PD 02-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-0501349.

XX

PR 31-JAN-2000; 2000US-179065P.

PR 04-FEB-2000; 2000US-180628P.

PR 24-FEB-2000; 2000US-184664P.

PR 02-MAR-2000; 2000US-186350P.

PR 16-MAR-2000; 2000US-189874P.

PR 17-MAR-2000; 2000US-190076P.

PR 18-APR-2000; 2000US-198123P.

PR 19-MAY-2000; 2000US-205515P.

PR 07-JUN-2000; 2000US-209457P.

PR 28-JUN-2000; 2000US-214886P.

PR 30-JUN-2000; 2000US-215135P.

PR 07-JUL-2000; 2000US-216647P.

PR 11-JUL-2000; 2000US-216880P.

PR 11-JUL-2000; 2000US-217487P.

PR 11-JUL-2000; 2000US-217496P.

PR 14-JUL-2000; 2000US-218290P.

PR 26-JUL-2000; 2000US-220963P.

PR 26-JUL-2000; 2000US-220964P.

PR 14-AUG-2000; 2000US-224518P.

PR 14-AUG-2000; 2000US-224519P.

PR 14-AUG-2000; 2000US-225213P.

PR 14-AUG-2000; 2000US-225214P.

PR 14-AUG-2000; 2000US-225266P.

PR 14-AUG-2000; 2000US-225267P.

PR 14-AUG-2000; 2000US-225268P.

PR 14-AUG-2000; 2000US-225270P.

PR 14-AUG-2000; 2000US-225447P.

PR 14-AUG-2000; 2000US-225757P.

PR 14-AUG-2000; 2000US-225758P.

PR 14-AUG-2000; 2000US-225759P.

PR 18-AUG-2000; 2000US-226279P.

PR 22-AUG-2000; 2000US-226681P.

PR 22-AUG-2000; 2000US-226686P.

PR 23-AUG-2000; 2000US-227182P.

PR 30-AUG-2000; 2000US-228924P.

PR 01-SEP-2000; 2000US-229287P.

PR 01-SEP-2000; 2000US-229343P.

PR 01-SEP-2000; 2000US-229344P.

PR 01-SEP-2000; 2000US-229345P.

PR 05-SEP-2000; 2000US-229509P.

PR 05-SEP-2000; 2000US-229513P.

PR 06-SEP-2000; 2000US-230437P.

PR 08-SEP-2000; 2000US-230438P.

PR 08-SEP-2000; 2000US-231242P.

PR 08-SEP-2000; 2000US-231243P.

PR 08-SEP-2000; 2000US-231244P.

PR 08-SEP-2000; 2000US-231413P.

PR 08-SEP-2000; 2000US-231414P.

PR 08-SEP-2000; 2000US-232080P.

PR 08-SEP-2000; 2000US-232081P.

PR 12-SEP-2000; 2000US-231968P.

PR 14-SEP-2000; 2000US-232397P.

PR 14-SEP-2000; 2000US-232398P.

PR 14-SEP-2000; 2000US-232399P.

PR 14-SEP-2000; 2000US-232400P.

PR 14-SEP-2000; 2000US-232401P.

PR 14-SEP-2000; 2000US-233063P.

PR 14-SEP-2000; 2000US-233064P.

PR 14-SEP-2000; 2000US-233065P.

PR 21-SEP-2000; 2000US-234223P.

PR 21-SEP-2000; 2000US-234274P.

PR 25-SEP-2000; 2000US-234997P.

PR 25-SEP-2000; 2000US-234998P.

PR 26-SEP-2000; 2000US-235484P.

PR 27-SEP-2000; 2000US-235834P.

PR 27-SEP-2000; 2000US-235836P.

PR 29-SEP-2000; 2000US-236327P.

PR 29-SEP-2000; 2000US-236367P.

PR 29-SEP-2000; 2000US-236368P.

PR 29-SEP-2000; 2000US-236369P.

PR 29-SEP-2000; 2000US-236370P.

PR 02-OCT-2000; 2000US-236802P.

PR 02-OCT-2000; 2000US-237037P.

PR 02-OCT-2000; 2000US-237038P.

PR 02-OCT-2000; 2000US-237039P.

PR 02-OCT-2000; 2000US-237040P.

PR 13-OCT-2000; 2000US-239935P.

PR 13-OCT-2000; 2000US-239937P.

PR 20-OCT-2000; 2000US-240960P.

PR 20-OCT-2000; 2000US-241221P.

PR 20-OCT-2000; 2000US-241785P.  
PR 20-OCT-2000; 2000US-241786P.  
PR 20-OCT-2000; 2000US-241787P.  
PR 20-OCT-2000; 2000US-241808P.  
PR 20-OCT-2000; 2000US-241809P.  
PR 20-OCT-2000; 2000US-241826P.  
PR 01-NOV-2000; 2000US-244617P.  
PR 08-NOV-2000; 2000US-246474P.  
PR 08-NOV-2000; 2000US-246475P.  
PR 08-NOV-2000; 2000US-246476P.  
PR 08-NOV-2000; 2000US-246477P.  
PR 08-NOV-2000; 2000US-246478P.  
PR 08-NOV-2000; 2000US-246523P.  
PR 08-NOV-2000; 2000US-246524P.  
PR 08-NOV-2000; 2000US-246525P.  
PR 08-NOV-2000; 2000US-246526P.  
PR 08-NOV-2000; 2000US-246527P.  
PR 08-NOV-2000; 2000US-246528P.  
PR 08-NOV-2000; 2000US-246532P.  
PR 08-NOV-2000; 2000US-246609P.  
PR 08-NOV-2000; 2000US-246610P.  
PR 08-NOV-2000; 2000US-246611P.  
PR 08-NOV-2000; 2000US-246613P.  
PR 17-NOV-2000; 2000US-249207P.  
PR 17-NOV-2000; 2000US-249208P.  
PR 17-NOV-2000; 2000US-249209P.  
PR 17-NOV-2000; 2000US-249210P.  
PR 17-NOV-2000; 2000US-249211P.  
PR 17-NOV-2000; 2000US-249212P.  
PR 17-NOV-2000; 2000US-249213P.  
PR 17-NOV-2000; 2000US-249214P.  
PR 17-NOV-2000; 2000US-249215P.  
PR 17-NOV-2000; 2000US-249216P.  
PR 17-NOV-2000; 2000US-249217P.  
PR 17-NOV-2000; 2000US-249218P.  
PR 17-NOV-2000; 2000US-249244P.  
PR 17-NOV-2000; 2000US-249245P.  
PR 17-NOV-2000; 2000US-249264P.  
PR 17-NOV-2000; 2000US-249265P.  
PR 17-NOV-2000; 2000US-249297P.  
PR 17-NOV-2000; 2000US-249299P.  
PR 17-NOV-2000; 2000US-249300P.  
PR 01-DEC-2000; 2000US-250160P.  
PR 01-DEC-2000; 2000US-250391P.  
PR 05-DEC-2000; 2000US-251030P.  
PR 05-DEC-2000; 2000US-251988P.  
PR 05-DEC-2000; 2000US-256719P.  
PR 06-DEC-2000; 2000US-251479P.  
PR 08-DEC-2000; 2000US-251856P.  
PR 08-DEC-2000; 2000US-251868P.  
PR 08-DEC-2000; 2000US-251869P.  
PR 08-DEC-2000; 2000US-251989P.  
PR 08-DEC-2000; 2000US-251990P.  
PR 11-DEC-2000; 2000US-254097P.  
PR 05-JAN-2001; 2001US-259678P.  
(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

DR WPI; 2001-476161/51.

DR P-PSDB; ABB10191.

XX Isolated nucleic acid molecule encoding an inflammation-associated  
PT polypeptide is used in preventing, treating or ameliorating a medical  
PT condition

PS Claim 1; SEQ ID NO: 79; 859pp + Sequence Listing; English.

XX The present invention provides human cDNAs, proteins and related genomic  
CC DNAs, these can be used in the treatment of neural, immune system,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal and proliferative disorders and inflammation. The present sequence

CC is a cDNA of the invention.

XX Sequence 993 BP; 218 A; 260 C; 328 G; 186 T; 1 other;

Query Match 6.1%; Score 95; DB 22; Length 993;  
Best Local Similarity 58.7%; Pred. No. 1e-13;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGATGCCAGCTTGCAGGCATCTTTCATCTGCTGCTTCCTTTGCTTCTCTCC 1078  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 780 TCCTGAAGCTGGCGGTCCTCCCAATCACCTCATCTGGCTCATCTTCTTCTACTGCTCTCC 721  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1079 ATTGCTGGCTCAAGCGCTTTCGCGAGATGCTACGATTTGGAGACAGAGATTTCTACCGGG 1138  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 720 ACTCTGCTGATGCTGGCTGCTGAGCTCATGCTGAGCTTTGGAGACCGGAGTTCTACCGGG 661  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1139 ACTGGTGGAACTCAACGCTCTTCTCCAACTACTACGCACCTGGGAACGTTGGTGGTCAATG 1198  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 660 ACTGGTGGAACTCCGAGTCTGTACCTACTTCTGGCAGAACTGGAACATCCCTTGTGCACA 601  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGCTGGCTTGTGCTGCTGCTGCTGCTGCTG 1258  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 600 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGCAGCAGCAAGT 547  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1259 GGTAGCCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1318  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 546 GGATGGCCAGGACAGGGGTGCTTCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 487  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1319 TCGTCTCTGGGTTCTTC 1335  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 486 TCCTCTGCGAATGTTTC 470  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

#### RESULT 15

AAV01533

ID AAV01533 standard; DNA; 1521 BP.

XX AC AAV01533;

XX DT 08-JUN-1998 (first entry)

XX Human acylcoenzyme A:cholesterol acyltransferase II DNA.

XX Acylcoenzyme A:cholesterol acyltransferase II; ARGP-1;  
KW ACAT related gene product 1; human; sterol esterification;  
KW inhibitor; atherosclerosis; hyperlipidaemia; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1224

FT /\*tag= a

XX WO9745439-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US09460.

XX PR 30-MAY-1996; 96US-0657620.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Sturley SL;

XX DR WPI; 1998-032573/03.

XX DR P-PSDB; AAW43406.

XX PT DNA encoding acylcoenzyme A: cholesterol acyltransferase II or  
PT III - useful to identify inhibitors for treatment of  
PT atherosclerosis or hyperlipidaemia  
XX Claim 5; Fig 15A-B; 121pp; English.



xx This isolated nucleic acid molecule encodes human acylcoenzyme  
 CC A:cholesterol acyltransferase II (see AAW43406), or ACAT related gene  
 CC product 1 (ARGP-1), that is expressed at high levels in intestine  
 CC and is a candidate for sterol esterification in these tissues. It  
 CC was identified following database searching for human ACAT-related  
 CC sequences and use of PCR and RACE to obtain full-length sequences.  
 CC An isolated nucleic acid (see AAV01534) for human ARGP-2 (see AAW43407)  
 CC was also identified. Also claimed are host vector systems for  
 CC production of ARGP polypeptides, and transgenic non-human mammals.  
 CC ARGP-1 and ARGP-2 nucleic acids can be used to diagnose or treat a  
 CC subject who has an imbalance in sterol levels due to a defect in  
 CC sterol esterification. A claimed oligonucleotide capable of  
 CC specifically hybridizing to a unique sequence of nucleotides in the  
 CC isolated nucleic acid molecule, or a vector expressing the  
 CC oligonucleotide, can be used to inhibit wild-type ARGP-1 or ARGP-2.  
 CC The wild-type enzymes can be used to identify an inhibitor, useful  
 CC in the treatment of atherosclerosis or hyperlipidaemia.  
 xx

xx SQ Sequence 1521 BP; 277 A; 489 C; 412 G; 343 T; 0 other;

Query Match 6.1%; Score 95; DB 19; Length 1521;  
 Best Local Similarity 58.7%; Pred. No. 1.2e-13;  
 Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

Qy 1019 TCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTCATCTCTTTGCCCTTCCTCC 1078  
 ||||| ||| ||| ||||| ||| ||||| ||||| ||||| |||||  
 Db 725 TCCTGAAGCTGGCGTCCCAATCACTCATCTGCTCATCTCTTCTACTGGCTCTTCC 784

Qy 1079 ATTGCTGGCTCAAGCCCTTTGCCGAGATGCTACGATTGGAGACAGATGTTCTACCGGG 1138  
 ||||| ||| ||| ||||| ||| ||||| ||||| ||||| |||||  
 Db 785 ACTCTGCCTGAATGCCGTGGCTGAGTCATGCAGTTTGGAGACCGGGAGTTCTACCGGG 844

Qy 1139 ACTGGTGGAACTCAACCTCCTTCTCCAACTACTACCGCACTTGAAGCTGGTGGTCCATG 1198  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 845 ACTGGTGGAACTCCGACTCTGTACCTACTTCTGGGAGAACTGGAACATCCCTGTGCACA 904

Qy 1199 ACTGGCTGTACAGCTAGTGTATCAGGATGGGCTGCGGCTCCTTTGGTGGCGGCGCCGAG 1258  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 905 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 958

Qy 1259 GGGTAGCCATGCTGGGTGTGTTCTCTCCGAGTCCGCGATGGCCCATGAGTATATCTTGTCT 1318  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 959 GGATGGCCAGGACAGGGGTGTCTCTGGCCTCGGCTTTCTTCCACGAGTACCTGGTGAGCG 1018

Qy 1319 TCGTCTGGGCTTCTTC 1335  
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 Db 1019 TCCCTCTGCGAATGTC 1035

Search completed: April 28, 2003, 08:30:55  
 Job time : 308 secs

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Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	1564.2	99.7	2040	3	US-09-165-042-4		Sequence 4, Appli
	2	405.6	25.9	4011	1	US-08-121-057-3		Sequence 3, Appli
	3	405.6	25.9	4011	2	US-08-509-187D-3		Sequence 3, Appli
	4	405.6	25.9	4011	2	US-09-121-396-3		Sequence 3, Appli
	5	405.6	25.9	4011	5	PCT-US93-09704A-3		Sequence 3, Appli
	6	359.8	22.9	4079	1	US-08-121-057-2		Sequence 2, Appli
	7	359.8	22.9	4079	2	US-08-509-187D-2		Sequence 2, Appli
	8	359.8	22.9	4079	2	US-09-121-396-2		Sequence 2, Appli
	9	359.8	22.9	4079	5	PCT-US93-09704A-2		Sequence 2, Appli
	10	134.6	8.6	996	1	US-08-121-057-1		Sequence 1, Appli
	11	134.6	8.6	996	2	US-08-509-187D-1		Sequence 1, Appli
	12	134.6	8.6	996	2	US-09-121-396-1		Sequence 1, Appli
	13	134.6	8.6	996	5	PCT-US93-09704A-1		Sequence 1, Appli
	14	95	6.1	1895	4	US-09-326-203A-14		Sequence 14, Appli
	15	95	6.1	1976	3	US-09-165-042-2		Sequence 2, Appli
	16	81.4	5.2	1650	4	US-03-103-754A-2		Sequence 2, Appli
	17	79.8	5.1	1766	4	US-09-326-203A-15		Sequence 15, Appli
	18	79.8	5.1	1766	4	US-09-326-203A-16		Sequence 16, Appli
	19	56.8	3.6	7218	1	US-08-232-463-14		Sequence 14, Appli
	20	55.4	3.5	519	4	US-09-326-203A-11		Sequence 11, Appli
	21	50	3.2	1942	3	US-09-326-203A-1		Sequence 1, Appli
	22	42	2.7	3358	3	US-09-248-571-2		Sequence 2, Appli
	23	42	2.7	3358	4	US-09-553-726-2		Sequence 2, Appli
C	24	41.2	2.6	7218	1	US-08-232-463-14		Sequence 14, Appli
	25	40	2.5	629	4	US-09-103-754A-3		Sequence 3, Appli
	26	39.8	2.5	2970	4	US-09-110-517-3		Sequence 3, Appli
	27	39.8	2.5	5173	1	US-08-242-677-1		Sequence 1, Appli
C	27	39.8	2.5	5173	1	US-08-242-677-1		Sequence 1, Appli



Db 1917 TGCTTATGCTTTTGGCAAAATTTCTACCGTTGTTGGACCTGGTGGATCATGTTCCTGT 1976  
QY 527 CCACCCCTGTTGGCGCCGTACAGGCCCTACGGCTGGCGGACGGGACACCTGGACGAGG 586,  
Db 1977 CTACATTTTCAGTTCCTATTTTCTGTTTCAACATTTGGCCACCTGGCTATAGCAAGATT 2036  
QY 587 CGAGGCGCTGGCGTGGCGCTTTTGGCGCCGACGCGGCTGGCTGCTGGCGCTGGCGG 646  
Db 2037 CTCATCGCTGATCGCTCTCTCTCCATGCTTTCTTTTCATGATCTTCCAGATTGGAG 2096  
QY 647 TCC-----AGTGGCGCTGGAGCATGACCTCCCGCGCGCTCCCGT 688  
Db 2097 TTTAGGTTTTGGACCAACAATATGTTGTATAGCATATACATGCCACAGCTTCCCGGT 2156  
QY 689 GTGCTCTGGTTCGACGAGTTAGGTTCTGATGAAGCTACTCTCTCTCTGAGAGAGG 748  
Db 2157 TCATCATATATTCGACGAGATTCGTTTGTATGAGGCCACCTCATTTGTTCAGAGAGA 2216  
QY 749 CTGTCCTGGGATCTTCGTCGACGAGGAGGTGAGGGGATCCAGGCCCTCCAGTTTCTCCA 808  
Db 2217 ACGTGCTCGGGTACTAAAT-TCAGCTAAGGAGAGAAATCAAGCACTGTTCCAATACCTACA 2275  
QY 809 G-----CTACCTCTACTTCTCTGCGCCACACTCATCTACAGGAGACTTACCT 861  
Db 2276 GTCAACAGATATTGTACTTCTTATTTGCTTACCTTATCTACCGTGTACCGTATATCCC 2335  
QY 862 AGGACGCCCTATGTGAGTGGAAATATGTCGCCAAGAACTTTGCCAGGCCCTGGGATGT 921  
Db 2336 AGAATCCCACTGTAGATGGGTATGTCGCTATGAAGTTTGCACAGGCTTTGGTTC 2395  
QY 922 GTGCTCTATGCCCTTCATCTCGGCGGCTCTGTCTCTCTGCTGCTTTGTCGCAACATGAGC 981  
Db 2396 TTTTCTCTATGTACTACATCTTTGAAAGGCTTTGTGCCCTGTTTTCGAATATCAAA 2455  
QY 982 CGAGAGCCCTTACGACCCGCTGCTGCTCTCTATCTCTGATGCCAGCTTGCAGG 1041  
Db 2456 CAGAGCCCTTACGCGCTGCTGCTGCTGCTATGTTTAACTCCATCTTTCGCCAGGT 2515  
QY 1042 ATCTTCATGCTGCTGCTATCTTTTGGCTTCTCTCATTGCTGGCTCAACGCCCTTGGC 1101  
Db 2516 GTGCTGATCTCTCTCTTCTTTTGGCTTTTGGACTGCTGGCTCAATGCTTTGCT 2575  
QY 1102 GAGATGCTAGATTGGAGACAGATTTCTTACCGGACTGGTGGAACTCAACGCTCTTC 1161  
Db 2576 GAGATGTTAGCTTTGGTGACAGATTTCTATGAAGATTGGTGAAGTCCACGCTATAC 2635  
QY 1162 TCCAACCTACTACGCACTTGGAGCTGCTGCTCCTACCTGCTGCTGCTACAGCTAGCTAT 1221  
Db 2636 TCCAACCTATATAGAACCTGGAATGCTGCTGCTGCTGCTGCTGCTATATTTACTATGCTTAC 2695  
QY 1222 CAGATGGGCTGGGCTCTTGGTGGCGGCGGAGGGGTAGCCATGCTGGGTGCTGCTC 1281  
Db 2696 AAGGACTTTCTGCTTTTCTCAAGAGATTTCAAACTGCTGCCATGTTAGCTGCTTT 2755  
QY 1282 CTGCTTCGCGAGTGGCCATGAGTATATCTTCTGCTGCTGCTGCTGGGTTCTTCTATCCC 1341  
Db 2756 GCTGTATCTGCTGATGACGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2815  
QY 1342 GTCATGCTGATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401  
Db 2816 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2875  
QY 1402 CGCACCGCGCGGATGGAAGCTGCTGATGTGGACCATGCTGTTCTTAGGCGAGGGAATC 1461  
Db 2876 CGGAAAGCGGATTTGGAATGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2935  
QY 1462 CAGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521  
Db 2936 TTAATCTGCTTTTATCTCAAGAATGATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2995  
QY 1522 ACTTTCGGGGCTGGTGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563  
Db 2996 ACATTTTGGATTTATGTCGGGCCACGTTTCTGGGACTTGTCTGT 3037

## RESULT 3

US-08-509-187D-3  
; Sequence 3, Application US/08509187D  
; Patent No. 5834283  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.  
; TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/509,187D  
; FILING DATE: 31-JUL-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lamport Hammitte, Ann  
; REGISTRATION NUMBER: 34,858  
; REFERENCE/DOCKET NUMBER: DCI-033cpdv  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4011 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1397..3046  
; US-08-509-187D-3

Query Match 25.9%; Score 405.6; DB 2; Length 4011;  
Best Local Similarity 58.9%; Pred. No. 1.1e-94;  
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

QY 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAGTCCCTTCATGAGCTGATGG 346  
Db 1737 CACCTCAGAAACAGAAAGATTTTATGCAAGCGCTCTCTTAGATGAAGCTGCTTG 1796  
QY 347 AGGTGACAGCATTTCCGACCATCTACCATGTTTCATCGCTGGCGTGTGTCTTCATCA 406  
Db 1797 AAGTGGACCATCAGAAATATATCATGTTTATTGCGCTCCTCATCTCTTATATCC 1856  
QY 407 TCAGCACCTGGCCATGACATTCATTGATGAGGCGAGCTGCTGCTGAGTTTGACCTAC 466  
Db 1857 TCAGCACATTTGTAGTATACATTGATGAAGAAAGCTGCTGTTGATGATGATGCTCC 1916  
QY 467 TGATCTTCAGCTTCGACAGCTGCATTTGGCGCTGGTGGCTGCTGCTGCTGCTGCTGCT 526  
Db 1917 TGTCTTATGCTTTTGGCAAAATTTCTTACCGTGTGTTGGACCTGGTGGATGATGCTTCT 1976  
QY 527 CCACCTGTTTGGCGCGGTACCAAGCCCTTACCGCTGTGGCGCCAGGGGACCTGGAGCGAG 586  
Db 1977 CTACATTTTCAGTTCCCTATTTTCTGTTTCAACATTTGCGCAGCTGCTATAGCAAGCT 2036  
QY 587 CGACGGGCTGGGCTGTGCGCTTTTATAGCCGCCACGCGGTGGTGTGCTGCGCGCTGCGCG 646











Db 2828 TATCTGCTAGTACAGAAATGCTTGGCTGTGCTTGGCTTTTCTATCCCGTGC 2887  
QY 1346 TGTGTATACCTCTCTTGTGTCATTTGAGGAAATGTTGAACCTTCATGATCATGACACGCGCA 1405  
Db 2888 TGTTCGTGCTCTTCATGCTTCTTGGATGCTTTCACATTCATGTCATGATAGTCGGA 2947  
QY 1406 CCGGCCCGCATGGAAGCTGCTGATGAGGACCATGCTGTTTCAGGCCAGGGAATCCAGG 1465  
Db 2948 AAAAGCCGATTTGGAATGTTCTGATGAGGACTTCTCTTTCTTTGGGCAATGGAGTCTTAC 3007  
QY 1466 TCAGCCTGTACTGCCAGAGTGTAGCACGCGGCGCACTCCCCCT 1510  
Db 3008 TCTGCTTTTATCTCAAGATGGTATGACGCTCGGCACGTGTACCT 3052

## RESULT 8

US-09-121-396-2

Sequence 2, Application US/09121396

Patent No. 5968749

GENERAL INFORMATION:

APPLICANT: CHANG, TA-YUAN

APPLICANT: CHANG, CATHERINE C. Y.

TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE &amp; COCKFIELD

STREET: 28 STATE STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/121,396

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/509,187

FILING DATE: 07/31/95

ATTORNEY/AGENT INFORMATION:

NAME: LAMPORT HAMMITTE, ANN.

REGISTRATION NUMBER: 34,858

REFERENCE/DOCKET NUMBER: DCI-033CPDV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-2700

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4079 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-121-396-2

Query Match 22.9%; Score 359.8; DB 2; Length 4079;  
Best Local Similarity 58.0%; Pred. No. 6.6e-83;  
Matches 722; Conservative 0; Mismatches 502; Indels 21; Gaps 4;

QY 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTGATGAGCTGATGG 346  
Db 1808 CACCTCCAGAACAGGAAAGATTTTATTGCAAGGCGCTCTCTCTAGATGAAGTCTTG 1867  
QY 347 AGGTGAGCATTTCCGACCATCTACCATGTTTATCGCTGGCCTGTGCTTCTATCA 406  
Db 1868 AGTGGACCACATCAGAACATATATCATATGTTATTGCCCCCTCTCTTATTC 1927

QY 407 TCAGCACCCCTGGCCATCGACTTCATTATGAGGCGAGGCTGCTGCTGG--AGTTTGACCT 464  
Db 1928 TCAGCACACTTGTAGTAGATTACATTGATGAAGAGGCTGGTGTCTTGAAGTTACGCT 1987  
QY 465 ACTG-ATCTTCAGCTTCGACAGCTGCCAATGGCGGTGTGACCTGGTGGCCCATGTTTC 523  
Db 1988 CTTGCTCTTATGCAATTTTGGCAATTTCTACCGTGTGTTGGACCTGGTGATCATGTTCC 2047  
QY 524 TGTCCACCCCTGTTGGCGCGTACCAGGCCCTACGGCTGTGGCGGAGGCGACCTTGACGC 583  
Db 2048 TGTCTACATTTTCAGTTCCTATTTCTGTTTCAACATTTGGGCACTGGCTATAGCAAGA 2107  
QY 584 AGCGACGGGCTGTGCTGTGGCTTTTAGCGGCCACCGCGTGTGCTGTGCGCCTGC 643  
Db 2108 GTTCTCATCCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 2167  
QY 644 CGGTCCACGTGGCG-----TGGAGCATCAGCTCCGCGGCGCTCCCGTTGT 690  
Db 2168 GAGTTCTAGGTTTGGACCAACATATGTTGTGTAGCATATCTGCCACAGCTTCCCGG 2227  
QY 691 GTCCTGCTCTCGAGCAGGTTAGTTCCTGATGAAAGCTACTCTCTCTGAGAGGCT 750  
Db 2228 TTTTCATATTATTCGACGACATGCTTTTGTAAAGGCCCACTCATTTGTCAGAGAAC 2287  
QY 751 GTGCTGGGATCCTTGTGCCAGAGAGTGAGGGGATCCAGGCC-----CCAGTTTCT 805  
Db 2288 GTGCTCGGTACTAATTCAGCTAAGGAGAAATCAAGCACTGTTCACATACCTACAGTCA 2347  
QY 806 CCAGCTACCTCTACTCTCTTCTGCCCAACACTCATCTACAGGAGACTTACCTAGCA 865  
Db 2348 ACAGTATTTGACTTCTTATTGCTCTCCACCCTTATCTACCGTGACAGCTATCCAGGA 2407  
QY 866 CGCCTATGTCAGGTGGAATATGTTGGCCAAGAACTTTGCCAGGCGCTTGGATGTGTC 925  
Db 2408 ATCCCACTGAAGTGGGTATGTTGCTATGAAGTTTGCACAGGCTTTTGTGTTGCTTT 2467  
QY 926 TCTATGCTGCTCATCTCCCTGGCGGCTCTGTGTTCTGCTCTTTGGCAACATAGCCGAG 985  
Db 2468 TCTATGCTGCTACATCTTTTGAAGGCTTTGTGCCCGCTTTGTCGAAATATCAACAGG 2527  
QY 986 AGCCCTTCAGCACCGCTGCCCTGCTCTCTATCTGATGCCAGTTCGCCAGGCTATCT 1045  
Db 2528 AGCCCTTCAGCGCTGCTGTTCTGGTCCATGTTATTTAACTCCATCTGCCAGGTGTC 2587  
QY 1046 TCATGCTGCTCATCTCTTTGCTTCTCCTCAATGCTGGCTCAACGCTTTGGCGAGA 1105  
Db 2588 TGATTCTCTCTCTTCTTTTGGCTTTTGGCTGCTGCTCAATGCTTTGCTGAGA 2647  
QY 1106 TGCTACGATTTGGAGACAGATGTTCTACCGGAGTGGTGAACATCAAGCTCTTCTCCA 1165  
Db 2648 TGTTAGCTTTGTCAGAGATGTTCTATAAGGATTTGGTGAACCTCCAGCTCATCTCCA 2707  
QY 1166 ACTACTACCGCACTTTGGAACGCTGGTGTCCATCACTGGCTGTACAGTACGTTATCAGG 1225  
Db 2708 ACTATTATAGAACCCTGGAATGTTGGTGTCCATGACTGGCTATATTACTATGTTACAAG 2767  
QY 1226 ATGGGCTGGGCTCCTTGGTGCCCGGCGGAGGGGTAGCCATGCTGGGTGTGTTCTG 1285  
Db 2768 ACTTCTCTGCTGTTTTCTTCAAGAGATTCAAAATCTGCTGCCATGTTAGTGTCTTTGCTG 2827  
QY 1286 TCTCCGAGTGGCCCATGAGTATATCTTCTGCTCTGCTGGGTTCTTATATCCGTC 1345  
Db 2828 TATCTGCTGTAGTACAGAAATGCTTGGCTGTGTTGCTTGTAGCTTTTCTATCCCGTGC 2887  
QY 1346 TGCTGATCTCTCTTCTGTCATTTGAGGAATGTTTGAACCTTCATGATGATGACGAGCA 1405  
Db 2888 TGTTCGCTCTCTCTATGTTCTTTGGAATGGCTTTCAACTTCATTGCTCAATGATAGTCGA 2947  
QY 1406 CGGCCCCGCAATGGAACGCTGCTGATGTGACCATGCTGTTTCTTAGCCAGGGAATCCAGG 1465  
Db 2948 AAAAGCCGATTTGGAATGTTCTGATGTGAGTCTCTCTTTTCTTGGCAATGAGTCTTAC 3007  
QY 1466 TCAGCTGTACTGCCAGGAGTGGTACGACAGGCGCACTGCCCT 1510

Db 3008 TCTGCTTTTATCTCAAGATGTTGATGACGCTCGGCACTGTACCT 3052  
|||||

## RESULT 9

PCT-US93-09704A-2

; Sequence 2, Application PC/TUS9309704A

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

; NUMBER OF SEQUENCES: 9

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/09704A

; FILING DATE: October 12, 1993

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. SER. NO. 959,950

; FILING DATE: October 14, 1992

; APPLICATION NUMBER: U.S. SER. NO. 121,057

; FILING DATE: September 10, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: LAMPORT HAMMITTE, ANN.

; REGISTRATION NUMBER: 34,858

; REFERENCE/DOCKET NUMBER: DCI-033CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-2700

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4079 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

PCT-US93-09704A-2

Query Match 22.9%; Score 359.8; DB 5; Length 4079;  
Best Local Similarity 58.0%; Pred. No. 6.e-83;  
Matches 722; Conservative 0; Mismatches 502; Indels 21; Gaps 4;

QY 287 CATCCCTGGGGAACACAAAGTTTTCATCATCCGCAAGTCCCTGCTGTGATGACGTGATGG 346  
|||||

Db 1808 CACCTCCAGAACACAGGAAGATTTTATTCGAAGCGCCTCTCTTAGATGAACCTGCTTG 1867  
|||||

QY 347 AGGTGCAGCATTTCCGACCATCTACACATGTTTCATCGCTGGCCTGTGTCTTCATCA 406  
|||||

Db 1868 AAGTGGACACATCAGAACATATACATGTTTATGGCCCTCCTCATCTCTTTATCC 1927  
|||||

QY 407 TCAGCACCTTGGCCATCGATTCATGATGAGGCGAGCTGCTGCTGG -- AGTTTGACCT 464  
|||||

Db 1928 TCAGCACACTGTAGTAGATTACATTCATGAAGGAAGGCTGGTCTGCAAGTTACGCC 1987  
|||||

QY 465 ACTG-ATCTTCAGCTTCGGACAGCTGCCATTTGGCGTGGTGGCTGACCTGGGTGCCATGTTTC 523  
|||||

Db 1988 CCTGTCTTATGCAATTTTGGCAAAATTTCCCTACCGTGTGTTGGACCTGGGTGATGTTCC 2047  
|||||

QY 524 TGTCCACCCCTGTGGCGCCCTACAGCCCTACGGCTGTGGCGCAGGGGACCTGGGACGC 583  
|||||

Db 2048 TGTCTACATTTTCAGTTCCTCTATTTCTGTTTCAACATTTGGCGCACTGGGTATAGCAAGA 2107  
|||||

QY 584 AGGCGAGGCGCCTGGGTGTGCGCTTTTACGCCGCCAGCGGCTGCTCTGGCGCTGC 643  
|||||

Db 2108 GTTCTCATCGCTGATCCGTTCTCTCTTCCATGCTTCTTTTCATGATCTTCCAGATTG 2167  
|||||

QY 644 CGGTCCACGTGGCGG -----TGGACATCAGTCCCGCGGCTCCCGTGT 690  
|||||

Db 2168 GAGTTCTAGTTTTGGACCAACATATGTTGTGTAGCATATCTCTGCCACCACTTCCCGG 2227  
|||||

QY 691 GTCTGTGCTTTCGAGCAGGTTAGGTTCTCTGATGAAAGCTACTCTCTCTGAGAGAGCT 750  
|||||

Db 2228 TTCAATCATTTATTCGAGCAGATCGTTTGTATGAAGGCCACTCATTTGTGAGAGAGAAC 2287  
|||||

QY 751 GTGCTGGGATCCTTCTGTCAGAGAGGTTGAGGGGATCCAGGCC -----CCCAGTTTCT 805  
|||||

Db 2288 GTGCTCGGTTACTTAATTCAGCTAAGGAGAAATCAAGCACTGTTTCCAAATACCTACAGTCA 2347  
|||||

QY 806 CCAGCTACCTCTACTCTCTCTGCCCCAACACACTCATCTACAGGAGAGACTTACCTCAGGA 865  
|||||

Db 2348 ACCAGTATTTGTTACTCTTATTTGCTCCTACCCCTATCTACCGTGACAGCTATCCAGGA 2407  
|||||

QY 866 CGCCCTATGTGAGGTGGAATATGTGCCCAAGAACTTTGCCAGGCCCTGGGATGTGTGC 925  
|||||

Db 2408 ATCCCACTGTAAGATGGGTTATGTTGCTATGAAGTTTGCACAGCTCTTTGGTTGCTTTT 2467  
|||||

QY 926 TCTATGCTGCTTCATCTCTGCGCCGCTCTGTGTGTTCTCTGCTGTTGCCAACATGAGCCGAG 985  
|||||

Db 2468 TCTATGTTACTACATCTTTGAAAGGCTTTGTGCCCCCTTTGTTTCGGAATATCAACAGG 2527  
|||||

QY 986 AGCCCTTCAGCACCCGCTGCTCTCTATCTGTCATGCCACGTTGCCAGGCACTCT 1045  
|||||

Db 2528 AGCCCTTCAGGCGCTGTTGCTGCTCTATGTGTATTAATCTTCTGTCAGGTTGCTG 2587  
|||||

QY 1046 TCATGCTGCTGCTCATCTCTTTTGGCTTCTCTCCATTTGCTGCTCAAGCCCTTTGCCGAGA 1105  
|||||

Db 2588 TGATCTCTCTCTTACTTTTTCCTTTTGGCACTGCTGCTCAATGCCCTTTGCTGAGA 2647  
|||||

QY 1106 TGCTACGATTTGGAGACAGGATGTTCTACCGGGAAGTGGTGAAGTCAAGCTCTCTCTCCA 1165  
|||||

Db 2648 TGTTCACGCTTTGGTGACAGGATGTTCTATAAGGATTTGGTGAAGTCCACGCTCATACTCCA 2707  
|||||

QY 1166 ACTACTACCGCACTTGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1225  
|||||

Db 2708 ACTATTAGAAGCTGGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2767  
|||||

QY 1226 ATGGGCTGCGGCTCCTTTGGTGCCCGCGGCGGAGGGGTAGCCATGCTGGGTGTTGTTCTCG 1285  
|||||

Db 2768 ACTTCTCTGCTTTTCTCCAAAGAGATTCAAAATCTGCTGCCATGTTAGCTGCTCTTTGCTG 2827  
|||||

QY 1286 TCTCCGAGTGGCCCATGATATATCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 1345  
|||||

Db 2828 TATCTGCTGATGACAGGAATATGCTTGGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2887  
|||||

QY 1346 TGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1405  
|||||

Db 2888 TGTTCGCTGCTCTCATGTTCTTTGGAAAGGCTTTTCAACTTCAATGCTCAATGATAGTCGGA 2947  
|||||

QY 1406 CCGGCGCGGCTGGAAGCTGCTGATGTGGACCATGCTGTTTCTAGGCGAGGAAATCCAGG 1465  
|||||

Db 2948 AAAAGCGATTTGGAATGTTCTGATGTGGACTTCTCTTTTCTTGGGCANTGGAGTCTTAC 3007  
|||||

QY 1466 TCAGCTGTTACTGCCAGGAGTGGTACGACGGGCGGCACTGCCCCCT 1510  
|||||

Db 3008 TCTGCTTTTATCTCAAGAAATGGTATGACGCTCGGCACCTGTACCT 3052  
|||||

## RESULT 10

US-08-121-057-1

; Sequence 1, Application US/08121057

; Patent No. 5484727

; GENERAL INFORMATION:

; APPLICANT: CHANG, TA-YUAN

; APPLICANT: CHANG, CATHERINE C. Y.

; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE &amp; COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MA

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/121,057  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: LAMPORT HAMMITTE, ANN.  
REGISTRATION NUMBER: 34,858  
REFERENCE/DOCKET NUMBER: DCI-033CP  
TELEPHONE: (617) 227-2700  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 996 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-121-057-1

Query Match 8.6%; Score 134.6; DB 1; Length 996;  
Best Local Similarity 53.1%; Pred. No. 2.6e-25;  
Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;

QY 287 CATCCCTGGGGAACAGAAAGTTTCATCATCCGAAAGTCCCTGCTGTATGAGCTGATGG 346  
DB 262 CACCTCCAGAACAGGAAGATTTTATGCAAGGGCGCTCTCTCTAGATGAAGCTGTTG 321  
QY 347 AGGTGACGATTTCCGACCATCTACACATGTTTCATCGCTGCGCTGTGCTTCATCA 406  
DB 322 AAGTGACCATCAAGAACATATATACATGTTTATTCGCCCTCCTCATCTCTTTATCC 381  
QY 407 TCAGCACCTTCCGACATCGACTTCATTGATGAGGCGAGGCTGCTGTGG--AGTTGACCT 464  
DB 382 TCAGCACATCTGTAGTAGATTACATTGATGAAGAGGCTGCTGTGAAGTTAGCCT 441  
QY 465 ACTG-ATCTTCAGTTCGGACAGCTGCCATTGCGCTGTGACCTGGTGGGCCCATCTTTC 523  
DB 442 CCTGCTTATGCAATTTGGCAATTTCTACCTGTTTGGACCTGGTGATCATCTTCC 501  
QY 524 TGTCACACCTGTGGGCGCTACAGGCGCTACGGCTGTGGGCGAGGGCACCTGGACGC 583  
DB 502 TGCTACATTTTCAGTTCCTCTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 561  
QY 584 AGCGAGGCGCTGGGCTGTGCGCTTTTAGCGCCCGACGCGGTGGTCTC-----633  
DB 562 GTTCTCATCGCTGATCCGTTCTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 621  
QY 634 ---TGCGCGCTCGGCTCCAGTGGCGGTGGAGCATCAGTCCGCGCGGCTCCCGTTGT 690  
DB 622 GAGTTCTAGTGTGGACCAACATATGTTGTGTAGCATATCTCTGCAAGGCTTCCCG 681  
QY 691 GTCTGTGCTTCGAGCAGGTAGTTCCTGATCAAAAGCTACTCTCTCTGAGAGAGGCT 750  
DB 682 TTCATCATTTTCGAGCAGATCGTTTGTATGAAGGCCCACTCATTTGTCAGAGAGAAC 741  
QY 751 GTGCTGGGATCTCTGTGCGACAGAGGTGAGGGGATCCAGGCC-----CCAGTTTCT 805  
DB 742 GTGCTCGGTACTATTACAGTAAGAGANAATCAAGCACTGTTCATACCTACAGTCA 801  
QY 806 CCAGCTACCTCTACTTCTCTCTGCGCCAACTATCTACAGGAGACTTACCCCTAGGA 865  
DB 802 ACCAGTATTTGTTCTTATTTGCTTCTTACCTTATCTACCGTGACAGCTATCCAGGA 861  
QY 866 CGCCCTATGTCAGTGAATTTGTGCCAAGAACTTTGCCAGGCGCTGGGATGTGTCG 925

Db 862 ATCCCACTCTAAGATGGGCTTATGTTGCTATGAAGTTTCCACAGGCTTTGGTGTCTTT 921  
QY 926 TCTATGCTGCTTCATCTGGCGCGCTCTGTGCTCTCTTTCCTTTCACATCAGCCGAG 985  
Db 922 TCTATGCTGCTACATCTTTGAAGGCTTTGTGCCCTTGTTCGGAATATCAACAGG 981  
QY 986 AGCCCTTCAGCACCC 1000  
Db 982 AGCCCTTCAGCGCTC 996

RESULT 11  
US-08-509-187D-1  
; Sequence 1, Application US/08509187D  
; Patent No. 5834283  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.  
; TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/509,187D  
; FILING DATE: 31-JUL-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lamport Hammitte, Ann  
; REGISTRATION NUMBER: 34,858  
; REFERENCE/DOCKET NUMBER: DCI-033cpdv  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 996 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-509-187D-1

Query Match 8.6%; Score 134.6; DB 2; Length 996;  
Best Local Similarity 53.1%; Pred. No. 2.6e-25;  
Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;

QY 287 CATCCCTGGGGAACAGAAAGTTTCATCATCCGAAAGTCCCTGCTGTATGAGCTGATGG 346  
DB 262 CACCTCCAGAACAGGAAGATTTTATGCAAGGGCGCTCTCTCTAGATGAAGCTGTTG 321  
QY 347 AGGTGACGATTTCCGACCATCTACACATGTTTCATCGCTGCGCTGTGCTTCATCA 406  
DB 322 AAGTGACCATCAAGAACATATATACATGTTTATTCGCCCTCCTCATCTCTTTATCC 381  
QY 407 TCAGCACCTTCCGACATCGACTTCATTGATGAGGCGAGGCTGCTGTGG--AGTTGACCT 464  
DB 382 TCAGCACATCTGTAGTAGATTACATTGATGAAGAGGCTGCTGTGAAGTTAGCCT 441  
QY 465 ACTG-ATCTTCAGTTCGGACAGCTGCCATTGCGCTGTGACCTGGTGGGCCCATCTTTC 523  
DB 442 CCTGCTTATGCAATTTGGCAATTTCTACCTGTTTGGACCTGGTGATCATCTTCC 501  
QY 524 TGTCACACCTGTGGGCGCTACAGGCGCTACGGCTGTGGGCGAGGGCACCTGGACGC 583  
DB 502 TGCTACATTTTCAGTTCCTCTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 561  
QY 584 AGCGAGGCGCTGGGCTGTGCGCTTTTAGCGCCCGACGCGGTGGTCTC-----633  
DB 562 GTTCTCATCGCTGATCCGTTCTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 621  
QY 634 ---TGCGCGCTCGGCTCCAGTGGCGGTGGAGCATCAGTCCGCGCGGCTCCCGTTGT 690  
DB 622 GAGTTCTAGTGTGGACCAACATATGTTGTGTAGCATATCTCTGCAAGGCTTCCCG 681  
QY 691 GTCTGTGCTTCGAGCAGGTAGTTCCTGATCAAAAGCTACTCTCTCTGAGAGAGGCT 750  
DB 682 TTCATCATTTTCGAGCAGATCGTTTGTATGAAGGCCCACTCATTTGTCAGAGAGAAC 741  
QY 751 GTGCTGGGATCTCTGTGCGACAGAGGTGAGGGGATCCAGGCC-----CCAGTTTCT 805  
DB 742 GTGCTCGGTACTATTACAGTAAGAGANAATCAAGCACTGTTCATACCTACAGTCA 801  
QY 806 CCAGCTACCTCTACTTCTCTCTGCGCCAACTATCTACAGGAGACTTACCCCTAGGA 865  
DB 802 ACCAGTATTTGTTCTTATTTGCTTCTTACCTTATCTACCGTGACAGCTATCCAGGA 861  
QY 866 CGCCCTATGTCAGTGAATTTGTGCCAAGAACTTTGCCAGGCGCTGGGATGTGTCG 925





RESULT 15  
US-09-165-042-2  
; Sequence 2, Application US/09165042  
; Patent No. 6100077  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L.  
; APPLICANT: Oelkers, Peter  
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL  
; TITLE OF INVENTION: ACYLTRANSFERASE  
; FILE REFERENCE: 0575/56331  
; CURRENT APPLICATION NUMBER: US/09/165,042  
; CURRENT FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1976  
; TYPE: DNA  
; ORGANISM: Yeast  
US-09-165-042-2

Query Match 6.1%; Score 95; DB 3; Length 1976;  
Best Local Similarity 58.7%; Pred. No. 5e-15;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;  
  
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DB 1212 TCCTGAAGCTGGCGGTCCCAATCACCTCATCTGGCTCATCTTCTACTGGCTCTTCC 1271  
  
QY 1079 ATTGCTGGCTCAAGCCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGG 1138  
DB 1272 ACTCCTGCCCTGAATGCCGTGGCTGAGCTCATGTCAGTTTGGAGACCGGGAGTTCTACCGGG 1331  
  
QY 1139 ACTGGTGAACCTAACCTCTCTTCCAACTACTACCCGACTTGGACGCTGGTGGTCCATG 1198  
DB 1332 ACTGGTGAACCTCGAGTCTGTACCTACTCTGGCAGAACTGGAACATCCCTGTGCACA 1391  
  
QY 1199 ACTGGCTGTACAGCTACGTATCAGGATGGCTGGGCTCCTTGGTGGCCGCGCCGAG 1258  
DB 1392 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 1445  
  
QY 1259 GGTAGCCATGCTGGGTGTGTTCTCTGCTTCCCGCAGTGGCCCATGAGTATATCTTCTGCT 1318  
DB 1446 GGATGGCCAGGACAGGGGTGTCTCTGGCCCTGGGCTTCTTCCACGAGTACCTGGTGAGCG 1505  
  
QY 1319 TCGTCTGGGGTCTTTC 1335  
DB 1506 TCCCTCTGCCAATGTTTC 1522

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OM nucleic - nucleic search, using sw model

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Title: US-09-918-026A-3

Perfect score: 1569

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Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	403.6	25.7	418	9	US-09-918-995-33158	Sequence 33158, A
2	391	24.9	399	9	US-09-918-995-33281	Sequence 33281, A
3	387.2	24.7	401	9	US-09-918-995-33355	Sequence 33355, A
4	386	24.6	402	9	US-09-918-995-33444	Sequence 33444, A
5	385.6	24.6	401	9	US-09-918-995-33843	Sequence 33843, A
6	384	24.5	393	9	US-09-918-995-33739	Sequence 33739, A
7	376.2	24.0	401	9	US-09-918-995-33159	Sequence 33159, A
8	350.6	22.3	365	9	US-09-918-995-34424	Sequence 34424, A
9	350.6	22.3	408	9	US-09-918-995-34099	Sequence 34099, A
10	338.2	21.6	383	9	US-09-918-995-35056	Sequence 35056, A
11	138.8	8.8	471	9	US-09-918-995-33288	Sequence 33288, A
12	95	6.1	993	10	US-09-764-853-79	Sequence 79, Appl
13	95	6.1	1411	9	US-10-273-438-1	Sequence 1, Appl
14	95	6.1	1895	9	US-10-157-855-14	Sequence 14, Appl
15	93.8	6.0	542	9	US-09-764-868-587	Sequence 587, Appl
16	92.4	5.9	774	9	US-09-764-868-279	Sequence 279, Appl
17	81.4	5.2	447	9	US-09-918-995-29256	Sequence 29256, A
18	81.4	5.2	452	10	US-09-867-701-4664	Sequence 4664, Appl
19	81.4	5.2	1650	9	US-10-273-438-3	Sequence 3, Appl

20	81.4	5.2	1650	9	US-10-273-438-9	Sequence 9, Appl
21	80	5.1	1122	9	US-09-774-639-29	Sequence 29, Appl
22	80	5.1	1122	9	US-09-969-730-58	Sequence 58, Appl
23	79.8	5.1	1766	9	US-10-157-855-15	Sequence 15, Appl
24	79.8	5.1	1766	9	US-10-157-855-16	Sequence 16, Appl
25	70.2	4.5	1572	9	US-10-223-076-17	Sequence 17, Appl
26	67.6	4.3	1181	9	US-10-223-076-16	Sequence 16, Appl
27	57.8	3.7	2099	9	US-10-223-076-12	Sequence 12, Appl
28	55.4	3.5	519	9	US-10-157-855-11	Sequence 11, Appl
29	54.2	3.5	471	9	US-09-918-995-1979	Sequence 1979, Ap
30	53.6	3.4	1964	9	US-10-223-076-14	Sequence 14, Appl
31	52.6	3.4	1537	9	US-10-223-076-4	Sequence 4, Appl
32	52.4	3.3	1446	9	US-10-223-076-6	Sequence 6, Appl
33	52.4	3.3	1512	9	US-10-223-076-8	Sequence 8, Appl
34	50	3.2	1904	9	US-10-223-076-2	Sequence 2, Appl
35	50	3.2	1942	9	US-10-157-855-1	Sequence 1, Appl
36	49	3.1	2090	9	US-10-223-076-10	Sequence 10, Appl
37	47.8	3.0	380	10	US-09-770-791-192	Sequence 192, App
38	45.8	2.9	433	10	US-09-764-853-314	Sequence 314, App
39	43.8	2.8	275	10	US-09-878-574-15694	Sequence 15694, A
40	41.8	2.7	790	9	US-10-123-155-204	Sequence 204, App
41	41.8	2.7	2802	10	US-09-815-242-7720	Sequence 7720, Ap
42	41.2	2.6	2715	9	US-09-712-363-101	Sequence 101, App
43	40.6	2.6	594	9	US-10-123-155-10	Sequence 10, Appl
44	40.6	2.6	1089	10	US-09-866-562-60	Sequence 60, Appl
45	40.6	2.6	1176	10	US-09-866-562-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1

US-09-918-995-33158

Sequence 33158, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 33158

LENGTH: 418

TYPE: DNA

ORGANISM: Homo sapiens

US-09-918-995-33158

Query Match 25.7%; Score 403.6; DB 9; Length 418;  
Best Local Similarity 99.0%; Pred. No. 3.4e-110;  
Matches 406; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1122	CAGGATGTTCTACGGGACTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG	1181
DB	9	CAGGATGTTCTACGGGACTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG	68
QY	1182	GAACGTTGGTGGTCCATGACTGGCTGTACAGTACGTTATCAGATGGGTGGGGTCTCT	1241
DB	69	GAACGTTGGTGGTCCATGACTGGCTGTACAGTACGTTATCAGATGGGTGGGGTCTCT	128
QY	1242	TGTTGCCGGGGCCGAGGGGTAGCCATGCTGGGTGTTCTTCTGCCAGTGGGCCCA	1301
DB	129	TGTTGCCGGGGCCGAGGGGTAGCCATGCTGGGTGTTCTTCTGCCAGTGGGCCCA	188
QY	1302	TGAGTATATCTTCTGCTCTCTCTCTGGGGTCTTCTATCCGCTCATGCTGATCTTCTCT	1361
DB	189	TGAGTATATCTTCTGCTCTCTCTCTGGGGTCTTCTATCCGCTCATGCTGATCTTCTCT	248
QY	1362	TGTCATTGGAGGAATGTTGAACCTTCATGATGCATGACACCGACCGCCCGCATGGAA	1421



Best Local Similarity 98.7%; Pred. No. 5.8e-105;  
Matches 389; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTCTACCGGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181  
Db 9 CAGGATGTTCTACCGGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCACTTG 68

Qy 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGTATCAGGATGGGCTCGGCTCCT 1241  
Db 69 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGTATCAGGATGGGCTCGGCTCCT 128

Qy 1242 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCTGCTCCGAGTGGCCCA 1301  
Db 129 TGGTCCCGGGCCGAGGGGTAAACATGCTGGGTGTCTTCTGCTCCGAGTGGCCCA 188

Qy 1302 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCTTCTATCCCGTCATGCTGATACTTCTTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCTTCTATCCCGTCATGCTGATACTTCTTCT 248

Qy 1362 TGTCAATGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 1421  
Db 249 TGTCAATGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 308

Qy 1422 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481  
Db 309 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368

Qy 1482 GGAGTGGTACGACGGCGGCACTGCCCTTACC 1515  
Db 369 GGAGTGGTACGACGGCGGCACTGCCCTTACC 402

RESULT 5  
US-09-918-995-33843  
; Sequence 33843, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33843  
; LENGTH: 401  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-33843

Query Match 24.6%; Score 385.6; DB 9; Length 401;  
Best Local Similarity 99.0%; Pred. No. 7.6e-105;  
Matches 388; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTCTACCGGGGACTGGTGAACCTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181  
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Qy 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGTATCAGGATGGGCTCGGCTCCT 1241  
Db 69 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGTATCAGGATGGGCTCGGCTCCT 128

Qy 1242 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCTGCTCCGAGTGGCCCA 1301  
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Qy 1302 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCTTCTATCCCGTCATGCTGATACTTCTTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCTTCTATCCCGTCATGCTGATACTTCTTCT 248

Qy 1362 TGTCAATGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 1421  
Db 249 TGTCAATGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 308

Qy 1422 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCTGCTCCGAGTGGCCCA 1481  
Db 309 TGGTCCCGGGCCGAGGGGAACCATGCTGGGTGTCTTCTGCTCCGAGTGGCCCA 188

Qy 1482 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCTTCTATCCCGTCATGCTGATACTTCTTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCTTCTATCCCGTCATGCTGATACTTCTTCT 248

Qy 1362 TGTCAATGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 1421  
Db 249 TGTCAATGGAGGAATGTTGAACCTTCAATGATCATGACAGCGCACCGCCCGCATGGAA 308

Qy 1422 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481  
Db 309 CGTCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368

Qy 1482 GGAGTGGTACGACGGCGGCACTGCCCTTACC 1513  
Db 369 GGAGTGGTACGACGGCGGCACTGCCCTTACC 400

RESULT 6  
US-09-918-995-33739  
; Sequence 33739, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33739  
; LENGTH: 393  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(393)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-33739

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Best Local Similarity 100.0%; Pred. No. 2.3e-104;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1182 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGTATCAGGATGGGCTCGGCTCCT 1241  
Db 69 GAACGTGGTGTCCATGACTGGCTGTACAGCTAGCTGTATCAGGATGGGCTCGGCTCCT 128

Qy 1242 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTCTTCTGCTTCGCACTGGCCCA 1301  
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Qy 1302 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCTTCTATCCCGTCATGCTGATACTTCTTCT 1361  
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; Sequence 33159, Application US/09918995
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; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33159
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-33159

Query Match 24.0%; Score 376.2; DB 9; Length 401;
Best Local Similarity 98.7%; Pred. No. 4.8e-102;
Matches 389; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1122 CAGGATGTTCTACCGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181
Db 9 CAGAGTTCTACCGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTG 68

QY 1182 GAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGTCGGCTCCT 1241
Db 69 GAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGTCGGCTCCT 128

QY 1242 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTCGGTCTCCGAGTGGCCCA 1301
Db 129 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTCGGTCTCCGAGTGGCCCA 188

QY 1302 TGAGTATATCTTCTGCTTCTGCTGGGTCTTCTATCCGTCATGCTGATCTTCTCT 1361
Db 189 TCAGTATATCTTCTGCTTCTGCTGGGTCTTCTATCCGTCATGCTGATCTTCTCT 248

QY 1362 TGTCTATGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATG 1421
Db 249 TGTCTATGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATG 308

QY 1422 CGTCTCATGTGGACCATGCTGTTCTTAGCCAGGGAATCCAGGTGACGCTGACTG 1478
Db 309 CGTCTCATGTGGACCATGCTGTTCTTAGCCAGGGAATCCAGGTGACGCTGACTG 365

RESULT 9
US-09-918-995-34099
; Sequence 34099, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34099
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-34099

Query Match 22.3%; Score 350.6; DB 9; Length 408;
Best Local Similarity 94.9%; Pred. No. 2e-94;
Matches 373; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1122 CAGGATGTTCTACCGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181
Db 15 CCGATTTTCTACCGGACTGGGGAACCTCAAGTCTTCTTCTCACTACTACCGCACTTG 74

QY 1182 GAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGTCGGCTCCT 1241
Db 75 GAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGTCGGCTCCT 134

QY 1242 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTCGGTCTCCGAGTGGCCCA 1301
Db 135 TGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTCGGTCTCCGAGTGGCCCA 194

QY 1302 TGAGTATATCTTCTGCTTCTGCTGGGTCTTCTATCCGTCATGCTGATCTTCTCT 1361
Db 195 TGAGTATATCTTCTGCTTCTGCTGGGTCTTCTATCCGTCATGCTGATCTTCTCT 254
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QY 1362 TGTCAATTGGAGGATGTTGAACCTTCATGACGATGACGACGACCGCCCGGCGATGAA 1421
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Db 255 TGTCAATTGGAGGATGTTGAACCTTCATGACGATGACGACGACCGCCCGGCGATGAA 314
|||||
QY 1422 CGTGTCTATGTGGACCATGTC-TGTTTCTAGGCGAGGAAATCCAGGTGAGCTGTACTGTCC 1480
|||||
Db 315 CAGCGTATGTGGACCATGCTGTTTCTATGCCAGGAAATTCAGGTGAGCTGTACTGTGC 374
|||||
QY 1481 AGAGTGTGACGACGCGCGCACTGCCCTTAC 1513
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Db 375 AAGAGTGGGACGACGCGCGCACTGGCCCTTAC 407
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RESULT 10
US-09-918-995-35056
; Sequence 35056, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35056
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(383)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-35056
Query Match 21.6%; Score 338.2; DB 9; Length 383;
Best Local Similarity 95.1%; Pred. No. 9.7e-91;
Matches 349; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1122 CAGGATGTTCTACCGGACGTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG 1181
|||||
Db 9 CAGGATGTTCTACCGGACGTGGTGAACCTCAACGCTCTCTCCAACTACTACCGCACTTG 68
|||||
QY 1182 GAAGTGTGTTCTACGCTAGCTGGTGTACAGCTAGCTATCAGGATGGGCTGGGCTCCT 1241
|||||
Db 69 GAAGTGTGTTCTACGCTAGCTGGTGTACAGCTAGCTATCAGGATGGGCTGGGCTCCT 128
|||||
QY 1242 TGTGTCGGGCGCGAGGGGTAGCATGCTGGGTGTCTCTGCTCCGAGTGGCCCA 1301
|||||
Db 129 TGTGTCGGGCGCGAGGGGTAAACATGCTGGGTGTGCTCTGCTCCGAGTGGCCCA 188
|||||
QY 1302 TGAGTATATCTTCGCTTCGCTCGGCGGTCTTCTATCCCGTATGCTGATCTTCCT 1361
|||||
Db 189 TGAGTATATCTTCGCTTCGCTCGGCGGTCTTCTATCCCGCATGCTGATCTTCCT 248
|||||
QY 1362 TGTCAATTGGAGGATGTTGAACCTTCATGACGATGACGACGACCGCCCGGCGATGAA 1421
|||||
Db 249 TGTCAATTGGAGGATGTTGAACCTTCATGACGATGACGACGACCGCCCGGCGATGAA 308
|||||
QY 1422 CGTGTCTATGTGGACCATGCTGTTTCTAGGCGAGGAAATCCAGGTGAGCTGTACTGTCCA 1481
|||||
Db 309 CGTGTCTATGTGGACCATGCTGTTTCTAGGCGAGGAAATCCAGGTGAGCTGTACTGTCCA 368
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QY 1482 GGAGTG 1488
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Db 369 CGAGTGG 375
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RESULT 11
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US-09-918-995-32388
; Sequence 32388, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32388
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(471)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32388
Query Match 8.8%; Score 138.8; DB 9; Length 471;
Best Local Similarity 92.4%; Pred. No. 2.4e-31;
Matches 146; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 883 AATTATGTGCCAAGAAGCTTTGCCAGGCCCTGGGATGTGCTCTATGCTTGCCTTCATC 942
|||||
Db 168 AGTTATGTGTCCTCCATGCCCTCCAGGCCCTGGGATGTGCTCTATGCTTGCCTTCATC 227
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QY 943 CTGGCGCGCTCTGCTGTTCTCTTGTCCCAACATGAGCCGAGAGCCCTTCAGCACCCGT 1002
|||||
Db 228 CTGGCGCGCTCTGCTGTTCTCTTGTCCCAACATGAGCCGAGAGCCCTTCAGCACCCGT 287
|||||
QY 1003 GCCTGTGTGCTCTATGCTGATGCGCACGTGGCCAGG 1040
|||||
Db 288 GCCTGTGTGCTCTATGCTGATGCGCACGTGGCCAGG 325
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RESULT 12
US-09-764-853-79/c
; Sequence 79, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-79
Query Match 6.1%; Score 95; DB 10; Length 993;
Best Local Similarity 58.7%; Pred. No. 3.6e-18;
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGATGCCACGCTTGCCAGGCATCTTCATGCTGCTGCTCTCTCTCTCTCTCTCTCC 1078
|||||
Db 780 TCCTGATGCCACGCTTGCCCAATCACCTCATCTGCTCTCTCTCTCTCTCTCTCTCTCC 721
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QY 1079 ATTGCTGGCTCAACGCTTTTGGCCGAGATGCTACGATTTGGAGACAGGATGTTGTACCGGG 1138
|||||
Db 720 ACTCTGCTGAATGCCGCTGGCTGAGCTCATGCTGAGAGCGGGAGTTCTACCGGG 661
|||||
QY 1139 ACTGTGGAACCTCAACGCTCTCTCCAACTACTACCGCACCTTGGAAACGCTGGTGGTCCATG 1198
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Db 660 ACTGGTGGAACTCGAGTCTGTACCTTCTGGCAGAACTGGAACATCCCTGTGCACA 601  
QY 1199 ACTGGCTGTACAGTACCTGTATCAGGATGGCTCGGCTCTTGTGGTCCGCGGCCGAG 1258  
Db 600 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGCGAGCAGCAAGT 547  
QY 1259 GGGTAGCCATGCTGGGTGTCTGTCTCCGAGTGGCCCATGAGTATATCTTCGCT 1318  
Db 546 GGATGGCCAGACAGGGGTGTTCTGTGCTCGGCTTCCTCCAGGAGTACCTGTGTAGCG 487  
QY 1319 TCGPCTCGGGTCTTTC 1335  
Db 486 TCCCTCTGCGAATGTTTC 470  
RESULT 13  
US-10-273-438-1  
; Sequence 1, Application US/10273438  
; Publication No. US20030072757A1  
; GENERAL INFORMATION:  
; APPLICANT: Farese, Robert V.  
; APPLICANT: Cases, Sylvaine  
; APPLICANT: Smith, Steven  
; APPLICANT: Erickson, Sandra  
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase  
; FILE REFERENCE: UCAL-105C1F2  
; CURRENT APPLICATION NUMBER: US/10/273,438  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US/10/040,315  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 60/107,771  
; PRIOR FILING DATE: 1998-11-09  
; PRIOR APPLICATION NUMBER: PCT/US98/17883  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 09/103,754  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 09/339,472  
; PRIOR FILING DATE: 1999-06-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-273-438-1  
Query Match 6.1%; Score 95; DB 9; Length 1411;  
Best Local Similarity 58.7%; Pred. No. 4.1e-18;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;  
QY 1019 TCTGTGATGCCAGTGGCCAGGCACTTTCATGCTGTGCTCATCTTCTTGTGCTTCTCTCC 1078  
Db 662 TCTGAAGCTGGGGTCCCAATCACCTCATCTGCTCATCTTCTTCTACTGCTCTTCC 721  
QY 1079 ATTGCTGGCTCAACGCTTTCGGAGATGCTAGGATTTGGAGACAGAGTGTCTACCCGG 1138  
Db 722 ACTCTTCCTGAAATCGGTGGTGGTCTCATGCTCATGCTCATGCTCATGCTCATGCTCATG 781  
QY 1139 ACTGGTGGAACTCAAGTCTTCTTCCAACTACTACCGCACTTGGAACTGGTGGTGCATG 1198  
Db 782 ACTGGTGGAACTCCGAGTCTGTACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 841  
QY 1199 ACTGGCTGTACAGTACGTGTATCAGGATGGGTGGGCTCTTGTGCTCCGCGGCCGAG 1258  
Db 842 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGCGAGCAGCAAGT 895  
QY 1259 GGGTAGCCATGCTGGGTGTCTTCTGCTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318  
Db 896 GGATGCCAGGACAGGGGTGTTCTGTGCTCGGCTTCCTCCAGGAGTACCTGGTGAGCG 955  
QY 1319 TCGTCTCGGGTCTTTC 1335  
Db 1199 TCGTCTCGGGTCTTTC 1335  
Db 1207 TCCCTCTGCGAATGTTTC 1223  
RESULT 15  
US-09-764-868-587  
; Sequence 587, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper

Db 956 TCCCTCTGCGAATGTTTC 972  
RESULT 14  
US-10-157-855-14  
; Sequence 14, Application US/10157855  
; Patent No. US20020170091A1  
; GENERAL INFORMATION:  
; APPLICANT: Lassner, Michael W.  
; APPLICANT: Ruzinsky, Diane M.  
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic  
; TITLE OF INVENTION: Acid Sequences  
; FILE REFERENCE: 16516.158  
; CURRENT APPLICATION NUMBER: US/10/157,855  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: 09/326,203  
; PRIOR FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: 60/088,143  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/108,389  
; PRIOR FILING DATE: 1998-11-12  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 1895  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (209)  
; OTHER INFORMATION: n at position 209 is unknown  
US-10-157-855-14  
Query Match 6.1%; Score 95; DB 9; Length 1895;  
Best Local Similarity 58.7%; Pred. No. 4.6e-18;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;  
QY 1019 TCTGTGATGCCAGTGGCCAGGCACTTTCATGCTGTGCTCATCTTCTTGTGCTTCTCTCC 1078  
Db 913 TCTGAAGCTGGGGTCCCAATCACCTCATCTGCTCATCTTCTTCTACTGCTCTTCC 972  
QY 1079 ATTGCTGGCTCAACGCTTTCGGAGATGCTAGGATTTGGAGACAGAGTGTCTACCCGG 1138  
Db 973 ACTCTTCCTGAAATCGGTGGTGGTCTCATGCTCATGCTCATGCTCATGCTCATGCTCATG 1032  
QY 1139 ACTGGTGGAACTCAAGTCTTCTTCCAACTACTACCGCACTTGGAACTGGTGGTGCATG 1198  
Db 1033 ACTGGTGGAACTCCGAGTCTGTACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 1092  
QY 1199 ACTGGCTGTACAGTACGTGTATCAGGATGGGTGGGCTCTTGTGCTCCGCGGCCGAG 1258  
Db 1093 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGCGAGCAGCAAGT 1146  
QY 1259 GGGTAGCCATGCTGGGTGTCTTCTGCTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318  
Db 1147 GGATGCCAGGACAGGGGTGTTCTGTGCTCGGCTTCCTCCAGGAGTACCTGGTGAGCG 1206  
QY 1319 TCGTCTCGGGTCTTTC 1335  
Db 1207 TCCCTCTGCGAATGTTTC 1223  
RESULT 15  
US-09-764-868-587  
; Sequence 587, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT232  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper



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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 04:51:57 ; Search time 1603 seconds

(without alignments)  
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Perfect score: 1569

Sequence: 1 atggagccagggggcccg.....cttggtcctgcatacctag 1569

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em\_estba:\*

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3: em\_estlin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estli:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402.4	25.6	799	13	BI222037 602935989
2	335.8	21.4	563	10	BE236762 145378 MA
3	298.2	19.0	778	13	BG920709 602824607
4	281.6	17.9	705	12	BG105735 602311957
5	272.6	17.4	992	12	BG674469 602620487
6	268	17.1	840	12	BG529751 602560622

7	264	16.8	893	9	AL527439	AL527439
8	246.2	15.7	694	9	AA867129	AA867129 vx23f11.r
9	245	15.6	741	12	BG696168	BG696168 602659280
10	241.6	15.4	731	9	AI049480	AI049480 ub37e11.r
11	240	15.3	300	9	AU099137	AU099137 AU099137
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13	233.8	14.9	887	9	AA867128	AA867128 vx23f10.r
14	227.6	14.5	635	17	AG133295	AG133295 Pan trogl
15	222.4	14.2	848	12	BG697784	BG697784 602661272
16	221.8	14.1	810	12	BF681650	BF681650 602155732
17	221.2	14.1	746	12	BG698372	BG698372 602658292
18	216.4	13.8	960	12	BG105756	BG105756 602311984
19	214	13.6	682	12	BG743201	BG743201 602634363
20	213.2	13.6	420	9	AA410072	AA410072 EST02151
21	204.4	13.0	484	10	AW466137	AW466137 BF230022A
22	204.2	13.0	553	10	BE013288	BE013288 123187 MA
23	202	12.9	878	14	BQ887458	BQ887458 AGENCOURT
24	200.2	12.8	608	9	AA867781	AA867781 vx16e09.r
25	197.6	12.6	500	12	BE861030	BE861030 UT-M-EP1-
26	186.2	11.9	601	14	BQ200762	BQ200762 UT-R-AB1-
27	185.2	11.8	915	12	BF968277	BF968277 602269663
28	183	11.7	460	14	R10272	R10272 yf36b09.r1
29	181.2	11.5	876	12	BF578775	BF578775 602094805
30	177.6	11.3	510	9	AI81841	AI81841 uh87h09.r
31	175	11.2	376	10	AW425878	AW425878 58867 MAR
32	171.8	10.9	655	10	BE026601	BE026601 db28h02.x
33	169.8	10.8	883	12	BG105795	BG105795 602312644
34	167.8	10.7	590	9	AL773907	AL773907 AL773907
35	162.4	10.4	639	13	BM485692	BM485692 pgm1c.pk0
36	148.4	9.5	612	10	BE025829	BE025829 db28h02.y
37	147.4	9.4	662	14	BQ521546	BQ521546 NISC.n111
38	147	9.4	801	12	BF130076	BF130076 601817955
39	143	9.1	385	10	BB872762	BB872762 BB872762
40	141.4	9.0	689	13	BJ016863	BJ016863 BJO16863
41	141.4	9.0	697	13	BJ019808	BJ019808 BJO19808
42	140.4	8.9	721	13	BJ028057	BJ028057 BJO28057
43	139.6	8.9	452	14	W76421	W76421 zd67e12.r1
44	139.6	8.9	668	13	BJ014628	BJ014628 BJO14628
45	139.4	8.9	467	14	R07295	R07295 yf14e10.r1

#### ALIGNMENTS

RESULT 1	BI222037	799 bp	mrna	linear	EST 11-JUL-2001
LOCUS	602935989F1	NCI_CGAP_Li9	Mus musculus	CDNA clone	IMAGE:5099063 5',
DEFINITION	mRNA sequence.				
ACCESSION	BI222037				
VERSION	BI222037.1				GI:14675481
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 799)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Sequencing by: The I.M.A.G.E. Consortium (LMNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov Plate: LMNL1238 row: b column: 24 High quality sequence start: 28 High quality sequence stop: 798.				
FEATURES	Location/Qualifiers				

source	1. 799	/organism="Mus musculus"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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```
BASE COUNT 139 a 155 c 153 g 258 t
ORIGIN
Query Match 17.9%; Score 281.6; DB 12; Length 705;
Best Local Similarity 64.2%; Pred. No. 3.1e-55;
Matches 439; Conservative 0; Mismatches 244; Indels 1; Gaps 1;
QY 843 CTACAGGGAGCTTACCCCTAGGAGCCCTATGTCAGGTGGAATATGTGCCAAGAACTT 902
DB 1 CTACCGGTGACAGCTATCCAGGAATCCCACTGTAAGATGGGTATGTGCTATGAAT 60
QY 903 TGCCAGGCCCTGGATGTGCTCTATGCTCTATGCTCTATGCTCTATGCTCTATGCT 962
DB 61 TGCACAGGTCTTTGGTGTCTTTCTATGCTCTATGCTCTATGCTCTATGCTCTATG 119
QY 963 TGTCTTTGGCAACATGAGCGGAGAGCCCTTCAGCACCCCTGCGCTGCTCTATGCT 1022
DB 120 CTGTTTGGGAATATCAACAGAGAGCCCTTCAGCGCTGCTGCTCTATGCTATG 179
QY 1023 GCATGCCAGTTGCCAGGATCTTCAGTGTGCTCTATGCTCTATGCTCTATGCTCT 1082
DB 180 TAACTCCATCTTCCAGGTGTGCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
QY 1083 CTGCTCAAGCCCTTGGCCGAGATCTAGATTTGGAGACAGATCTTACCGGACTG 1142
DB 240 CTGCTCAATGCTTCTGAGATGTTACGCTTTGTGACAGATGTTCTATAAGGATG 299
QY 1143 GTGGAATCAACCTCTCTTCCAACTACTACCGCACTTGGAGCTGGTGTCCATGACTG 1202
DB 300 GTGGAATCCACGTATCACTCCAACTATATAGAACCTGGAATGTGTTGCTCATGCTG 359
QY 1203 GCTGTACAGTACGTATACAGATGGGTGGGCTCTCTGCTCTCTCTCTCTCTCTCT 1262
DB 360 GCTATATTAATGCTTACAGAACTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 419
QY 1263 AGCATGCTGGGTGCTCTCTGCTCTCCAGTGGCCCATGAGTATATCTCTGCTCTCT 1322
DB 420 TGCCATGTAGTCTCTTCTGCTATCTGCTGTAGTACAGAAATGCTCTGCTCTCTCT 479
QY 1323 CTGCGGTCTCTCTATCCGCTCATGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 1382
DB 480 CTGAGCTTTCTATCCCGTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 539
QY 1383 CTTCATGATGATGACAGCGGACCGCCGCGGATGGAAGCTGCTGATGTGACCATGCT 1442
DB 540 CTTCATGTCAATGATGATGCGGAAAGCGGATTTGGAATGTCTGATGTGACCTCTCT 599
QY 1443 GTTCTTAGCCAGGAAATCCAGTCAAGCTGCTACTGCCAGGAGTGTACGCGCGGCA 1502
DB 600 TTTCTTGGCAATGGAGTCTTACTCTGCTTTTATCTCAAGATGATGATGACGCTCAG 659
QY 1503 CTGCCCCCTTACCCCGGCAACTTT 1526
DB 660 CTGCTCTCTGAAAAATCCCAATTT 683

RESULT 5
BG674469
LOCUS 602620487F1 NCI_CGAP_Skn3 Homo sapiens cdna clone IMAGE:4746069 5',
DEFINITION mRNA sequence.
ACCESSION BG674469
VERSION BG674469.1 GI:13905865
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 992)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10593 row: n column: 22  
High quality sequence stop: 828.  
location/Qualifiers

FEATURES  
source

1. .992  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4746069"  
/clone\_lib="NCI\_CGAP\_Skn3"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 199 a 216 c 231 g 346 t  
ORIGIN

Query Match 17.4%; Score 272.6; DB 12; Length 992;  
Best Local Similarity 63.2%; Pred. No. 4.6e-53;  
Matches 419; Conservative 0; Mismatches 244; Indels 0; Gaps 0;  
QY 901 TTTGCCAGCCCTGGATGTGCTCTATGCTGCTCTATGCTGCTCTATGCTGCTCTCTCT 960  
DB 2 TTTGCACAGCTCTTGGTGTCTTTCTATGTACTACATCTTTGAAGGCTTTGTGCC 61  
QY 961 CCTGTCTTTGCCAATGAGCGGAGAGCCCTTCAGCACCCGCTGCTGCTCTCTATC 1020  
DB 62 CCTGTCTTTGCCAATATCAACAGAGAGCCCTTCAGCGCTGCTGCTCTCTATGTA 121  
QY 1021 CTGATGCCAGCTTGCAGGATCTTCATGCTGCTGCTCTCTCTCTCTCTCTCTCTCT 1080  
DB 122 TTTAACTCCATCTTGCAGGCTGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 181  
QY 1081 TGTGCTCAACGCCCTTTCGCGAGATGCTACGATTTGGAGACAGAGATGTTCTACCGG 1140  
DB 182 TGTGCTCAATGCCCTTTCGCTGAGATGTTACGCTTTGGTGACAGAGATGTTCTATAAG 241  
QY 1141 TGTGGAATCAACGCTCTCTTCCAACTACTACCGCACTTGGAACTGCTGCTCTCTATG 1200  
DB 242 TGTGGAATCCACGCTACTCTCAACTATATAGAACCTGGAATGCTGCTGCTCTCTATG 301  
QY 1201 TGTGCTACAGTACGCTATCAGGATGGGCTGCGGCTCTCTGCTGCTGCTGCTGCTG 1260  
DB 302 TGTGCTATATCTATCTCTTACAAGGACTTTCTCTGCTTTTCTCCAAGAGATTCAAAT 361  
QY 1261 GTAGCCATGCTGGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
DB 362 GCTGCCATGTTAGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421  
QY 1321 GTCTCTGGGTTCTCTATCCCTCATGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 1380  
DB 422 TGTCTGAGCTTTTCTATCCCGTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 481  
QY 1381 AACTTCATGATGATGACAGCGCACCGCCGCGGATGGAACGCTGCTGATGTGGACCATG 1440  
DB 482 AACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 541  
QY 1441 CTGTTCTAGCGCAGGAAATCCAGGTCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
DB 542 CTCTTCTTGGGCAATGGAGTCTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 601  
QY 1501 CACTGCCCTTACCAGGCAACTTTTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
DB 602 CACTGCTCTCTCAAAATCCACATTTTGGATATGTCGCCGCCAGCTTCTCTGCTGCT 661  
QY 1561 CAT 1563

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Db 662 CGT 664

RESULT 6
BG529751
DEFINITION 602560622F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4698748 5',
            mRNA sequence.
            linear EST 03-APR-2001
            840 bp mRNA
ACCESSION BG529751
VERSION BG529751.1 GI:13521288
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 840)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cgaaps-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1CMI529 row: k column: 05
            High quality sequence stop: 764.
            Location/Qualifiers
                1..840
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:4698748"
                    /clone_lib="NIH_MGC_61"
                    /tissue_type="embryonal carcinoma"
                    /lab_host="DH10B (T1 phage-resistant)"
                    /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                    Sf11 (99ccctatgccc); Site_2: Sf11 (99ccctatgccc);
                    Double-stranded cDNA was prepared from cell line RNA. 5'
                    and 3' adaptors were used in cloning as follows: 5'
                    adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
                    sequence: 5'-ATTCTAGCGCCGAGCGGCGACATG-dT(30)BN-3'
                    (where B = A, C, or G and N = A, C, G, or T). Average
                    insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
                    contained inserts by PCR. This library was enriched for
                    full-length clones and was constructed by Clontech
                    Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                    Library."
BASE COUNT 163 a 195 c 178 g 304 t
ORIGIN

Query Match 17.1%; Score 268; DB 12; Length 840;
Best Local Similarity 63.4%; Pred. No. 5.1e-52;
Matches 460; Conservative 0; Mismatches 260; Indels 6; Gaps 3;

Qy 811 TACCTCTACTTCCCTCTCTGCCAACACTGATCTACAGGGAGACTTACCCTAGAGCGCC 870
Db 12 TATTGTACTTCTTATTGGCTTCTTACCCTTATCTACCGTGACAGCTATCCAGGAATCCC 71
Qy 871 TATGTACAGTGAATATATGGCCCAAGAACTTGGCCAGGCCCTGGGATGTGCTCTAT 930
Db 72 ACTGTAAGATGGGTATATGCTATGAAGTTTGACAGGTCCTTGGTGTCTTCTTAT 131
Qy 931 GCCTGCTTCACTCCRGCGCGCCTCTGTGCTCTGCTTCTTCCCAACATGAGCGGAGGCC 990
Db 132 GTGTACTACATCTTTGAAAGGCTTTGTGCCCCCTTGTTCGGAATATCAACAGAGGCC 191
Qy 991 TTCAGACCCCGTCCCGTGTCTCTATCTGATGCCAGCTGCGCAGGATCTTCAATG 1050
Db 192 TTCAGCGCTCGTGTCTGCTCTATGTGTATTTAACTTCCATCTTCCAGGTGTGCTGAT 251

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Qy 1051 CTGCTGCTCA-TCTTCTTTGCTTCTCCTCAATTGCTGGCTCAAGCGCTTTGGCGAGATGCT 1109
Db 252 CTCTTCTCTACTTTTCTTTGCTTCTTTCGACTGCTGGCTCAATGCTTTGCTGAGATGTT 311
Qy 1110 ACGATTGAGACAGAGATGTTCTACCGGAGCTGGTGGAACTCAACGCTCTCTTCCAACTA 1169
Db 312 ACGCTTTGTCAGAGATGTTCTATAAGGATTTGGTGGAACTCCACGTCATATCCAACTA 371
Qy 1170 CTACCGCACTTTGGAACGCTGGTGGTCCATGACTGGCTGTACAGCTACGTTATCAGGATGG 1229
Db 372 TTATAGAACCTGGAATGTTGGTGGTCCATGACTGGCTATATTACTATGCTTACAGGACTT 431
Qy 1230 GCTGGCGCTCTGCTGGTCCCGGCGGAGGAGTACCCATGCTGGGTGTGTTCTCTGCTCTC 1289
Db 432 TCTCTGGTTTTTCTCCAAAGATTCAAATCTGCTGCCATGTTAGCTGTCTTTGCTGTATC 491
Qy 1290 CGCAGTGGCCCATGAGTATATCTTCTGCTGCTGGTGGTCTTCTATCCCGTCACTGCT 1349
Db 492 TGTCTAGTACACGAATATGCTTGGCTGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 551
Qy 1350 GATACTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1408
Db 552 CGTCTCTCTCAATGTTCTTGGAAATGGCTTCAACCTCATGTTCAATGATAGTGGACACA 611
Qy 1409 GCCCGCATGGAACCTGCTGATGAGCACCATGCTTCTTAGCCAGGAA-----TCCAG 1464
Db 612 ACCGATTTGGAAATGCTGCTGATGAGCTTCTTCTTCTTGGCAATGGGAGCTCTTACCT 671
Qy 1465 GTCAGCCTGTACTGCCAGAGTGTGTACGACGGGGGACTGCCCTTACCCAGGCACT 1524
Db 672 CTGCTTTTATTTCTTCCCTCACGAATGGTATGACGCTCAGCACTGTCTCTGAAAAATCCC 731
Qy 1525 TTCCTGG 1530
Db 732 TTTTGG 737

RESULT 7
AL527439
LOCUS AL527439 893 bp mRNA linear EST 13-FEB-2001
DEFINITION AL527439 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC021YJ22 5
prime, mRNA sequence.
ACCESSION AL527439
VERSION AL527439.1 GI:12790932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS Li, W.B.; Gruber, C.; Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
            Location/Qualifiers
                1..893
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="CS0DC021YJ22"
                    /clone_lib="LTI_NFL003_NBC3"
                    /sex="male"
                    /tissue_type="neuroblastoma cells"
                    /lab_host="DH10B"
                    /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                    was primed with a NotI-oligo(dT) primer. Five prime end
                    enriched, double-stranded cDNA was digested with Not I and
                    cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                    vector. Library was normalized. Library was constructed
                    by Life Technologies. Contact : Feng Liang Life

```

AA867129	AA867129	694 bp	mRNA	linear	EST 16-MAR-1998
LOCUS					
DEFINITION	vx23f11.r1 Soares_thymus.2NDMT Mus musculus cDNA clone IMAGE:1265325 5' similar to gb:142293 Mus musculus acyl-coenzyme A:cholesterol acyltransferase (MOUSE);, mRNA sequence				

**KEYWORDS** EST. house mouse.  
**SOURCE** Mus musculus  
**ORGANISM** Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

**AUTHORS**  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Therrell, B.; Wylie, I.; Lennon, S.; Soares, P.; Wilson, R. and Waterston, R.

TITLE The WashU-RHMI Mouse EST Project  
JOURNAL Unpublished (1996)

COMMENT	CONTACT: MARRA M/MOUSE EST PROJECT	WASHU-HHMT MOUSE EST PROJECT

Washington University School of Medicine  
444 Forest Park Parkway Box 8501 St Louis MO 63108

Tel: 314 286 1800

Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)

THIS CLONE IS AVAILABLE REPEATED FREE THROUGH THE  
IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 441.

```
source
1. .694
/organism="Mus musculus"
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/strain="C57BL/6J"  
/file_name="tumor_10000"
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/clone="IMAGE:1265325"
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/sex="male"

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/usr/local/bin/cisco_cisco /dev_stage="4 weeks"
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/rad_host= dn10b
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
```

**polylinker; site\_1:** Not I; **site\_2:** EcoRI." ISC strand connect

TGTTACCAATCTGAAGTGGAGCGCCGGTTTTTTTTTTTTTT  
3' l double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

provided by Dr. Bertrand Jordan. Library went through two

Soares and M. Fatima Bonaldo."

BASE COUNT	130 B	170 C	103 G	224 L	4 OTHERS
ORIGIN					

Query Match 15.7%: Score 246.2: DB 9: Length 694;

Best Local Similarity	63.48;	Pred: No. 5.9e-47;			
Matches	277;	Conservative	0;	Mismatches	218;
				Indels	0;
				Gaps	0;

[illegible]

69

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[illegible][illegible]

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Qy 1116 TGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCAATACTACCG 11/5

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182 TGGTGACAGGATGTTTATAGGACTGGTGAACCTTACATCATCTCCAACTACTACAG 241
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1236 GCTCTTGGTGGCCGGCCGAGGGGTAGCCATGCTGGGTGTGTCTCTGCTCCGCGAGT 1295
302 GTTTTCTCGAAGAGTTTCAAACTCGCGCCATGCTGGCCGTCTCGCCCTGCGGCTGT 361
1296 GGCCCATGAGTATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1355
362 GGTGACGAGTATGCTTGGCCATGCTGCTGAGTACTTCTACGCGGTGCTCTTCTGCT 421
1356 CTTCTTGTCTATGAGGAAATGTTGAATCTCATGATCATGATGATGATGATGATGATGAT 1415
422 CTTCTATGCTTCTGGAATGCTTTAACTTCAATGTTAAAGACAGTCCGAAAGGCCAAT 481
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482 CTCGAACATCAGGCTTTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTA 541
1476 CTGCGAGAGTGGTACGAGCGGCGACTGCCCCCTTACCCAGGCACTTTCTGG 1530
542 GTCTCAAGAGTGGTATGCCGCCAGCACTGTCATCTGAAGAAACCTACATTTCTGG 596

RESULT 9
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DEFINITION mRNA sequence.
ACCESSION BG696168
VERSION BG696168.1 GI:13961039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NTH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10696 row: p column: 20
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Average insert size 1.5kb. Library constructed by Life
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QY 962 CTGTCTTTGCCAATCAGGCGAGAGCCCTTACGACCCGCTGCTGTCTCTATACC 1021
DB 72 CTTTGTTCGGAATATCAACACAGGAGCCCTTCAGCGCTCGTGTCTGCTCTATGTGAT 131
QY 1022 TGCATGCCACGTTGCCAGGCACTTTCATGCTGCTCATCTTCTTGGCCTTCCTCAT 1081
DB 132 TTAATCTCCATCTTCCAGGCTGCTGATCTCTTCTTCTTCTTCTTCTTCTTCTTCT 190
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DB 191 GCTGGCTCAATGCTTTGCTGAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGAT 250
QY 1142 GGTGGAATCAAGCTCTTCTTCCAACTACTACGCACTTGAAGCTGGTGTGCTCATGACT 1201
DB 251 GGTGGAATCCACGCTCATCTTCCAACTATATAGAACCTGGAATGCTGGTGTGCTCATGACT 310
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DB 431 GCTTGGAGCTTTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
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QY 1442 TGTTCTTAGCGAGGAGTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
DB 551 TTTTCTTGGGCAATGGAGTCTTACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 610
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DB 611 ACTGCTCTCTGAAAAATCCCACTTTTGG 639

RESULT 10
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DEFINITION AI049480 731 bp mRNA linear EST 08-JUL-1998
ub37ell.r1 Soares_thymus_2NBMT Mus musculus cDNA clone
IMAGE:1379948 5' similar to gb:L21934 STEROL O-ACYLTRANSFERASE
(HUMAN); gb:L42293 Mus musculus acyl-coenzyme A:cholesterol
acyltransferase (MOUSE);, mRNA sequence.
ACCESSION AI049480
VERSION AI049480.1 GI:3297767
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 731)
AUTHORS Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

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ACCESSION	AW099137		
VERSION	AW099137.1	GI:13550266	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Ekuryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 300) Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo K., Suyama,A. and Sugano,S.		
TITLE	In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by oligo-capping method		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,A.		

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RESULT 12
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DEFINITION BG500675.1 GI:13462192
ACCESSION BG500675
VERSION BG500675.1
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SOURCE human.
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  602547086F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4669480 5',
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  BG500675,
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  human.

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BG500675  
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 DEFINITION  
 BG500675 846 bp mRNA linear EST 27-MAR-2001  
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 mRNA sequence.  
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 VERSION  
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 KEYWORDS  
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 human.







http://image.llnl.gov  
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Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
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Query Match 14.28; Score 222.4; DB 12; Length 848;  
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Db 124 ACTCACGCTCATCTCCAACTATTATAGAACCTGGAATGTGGTGGTCCATGACTGGCTAT 183  
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